

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2005, 08:35:14 ; Search time 226.736 Seconds  
(without alignment)  
3517.904 Million cell updates/sec

Title: US-10-674-540A-1  
Perfect score: 1537  
Sequence: 1 gcaacgacccatcccaaac.....ctagcttaaaaaaaaaa 1537

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 8336576

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA-New:\*  
1: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
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9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
Score greater than or equal to the score of the result being printed.  
Psd is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	50.8	3.3 305312	US-10-995-561-13236	Sequence 13236, A
2	45.2	2.9 158692	US-11-121-086-30	Sequence 30, Appl
3	45	2.9 20190	US-10-995-561-13303	Sequence 13303, A
4	44.6	2.9 119036	US-10-995-561-13314	Sequence 13314, A
5	43.8	2.8 176002	US-11-121-086-25	Sequence 25, Appl
6	43.6	2.8 110000	US-11-155-492-1	Sequence 1, Appl
7	43.6	2.8 138054	US-11-121-086-96	Sequence 96, Appl
8	43	2.8 98716	US-10-995-561-13331	Sequence 13331, A
9	42.4	2.8 513	US-10-793-626-1925	Sequence 1925, Ap
10	42.4	2.8 176002	US-10-793-626-3425	Sequence 3425, Ap
11	42.4	2.8 176002	US-11-121-086-25	Sequence 25, Appl
12	42	2.7 1659	US-10-750-185-64246	Sequence 64246, A
13	41.8	2.7 4063	US-10-750-185-46813	Sequence 46813, A
14	41.8	2.7 105550	US-10-995-561-13235	Sequence 13235, A
15	41.6	2.7 1553	US-10-750-185-38081	Sequence 38081, A
16	41.6	2.7 153142	US-11-121-086-27	Sequence 27, Appl
17	41.4	2.7 1496	US-10-750-185-43143	Sequence 43143, A
18	41.4	2.7 150437	US-11-112-908-44	Sequence 44, Appl
19	41.4	2.7 150491	US-11-112-908-46	Sequence 46, Appl
20	41.4	2.7 172543	US-11-121-086-6	Sequence 6, Appl
21	41.4	2.7 182314	US-11-112-908-45	Sequence 45, Appl
22	41.4	2.7 611587	US-11-117-187-209	Sequence 209, Appl
23	41.2	2.7 159781	US-11-121-086-92	Sequence 92, Appl

C	24	41	2.7	1292	6	US-10-750-185-55224	Sequence 55224, A
	25	40.8	2.7	201	6	US-10-995-561-25865	Sequence 25865, A
	26	40.4	2.6	1011	6	US-10-750-185-26541	Sequence 26541, A
	27	40.4	2.6	103931	7	US-11-117-187-193	Sequence 193, App
	28	40.2	2.6	146656	7	US-11-121-086-68	Sequence 68, Appl
	29	39.8	2.6	3127	6	US-10-793-626-3776	Sequence 3776, Ap
	30	39.8	2.6	3157	6	US-10-793-626-2668	Sequence 3668, Ap
	31	39.6	2.6	340000	7	US-11-102-978-3	Sequence 3, Appl1
	32	39.6	2.6	1082144	7	US-11-117-187-211	Sequence 211, App
	33	39.4	2.6	1490	6	US-10-750-185-46942	Sequence 46942, A
	34	39.4	2.6	5592	7	US-11-192-967-5	Sequence 5, Appl1
	35	39.4	2.6	5592	7	US-11-193-715-5	Sequence 5, Appl1
	36	39.4	2.6	184868	7	US-11-121-086-88	Sequence 88, Appl1
	37	39.4	2.6	1082144	7	US-11-117-187-211	Sequence 211, App
	38	39.2	2.6	2036	6	US-10-995-561-13313	Sequence 13313, A
	39	39.2	2.6	54946	6	US-10-995-561-13479	Sequence 13479, A
	40	39.2	2.6	126552	7	US-11-121-086-1	Sequence 1, Appl1
	41	39.2	2.5	2162	6	US-10-750-185-40667	Sequence 40667, A
	42	39	2.5	3001	7	US-11-145-703-204	Sequence 204, App
	43	39	2.5	148220	7	US-11-121-086-90	Sequence 90, Appl
	44	39	2.5	153142	7	US-11-121-086-27	Sequence 27, Appl
	45	39	2.5	153142	7	US-11-121-086-27	Sequence 27, Appl

#### ALIGNMENTS

```
RESULT 1
US-10-995-561-13236/C
; Sequence 13236, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13236
; LENGTH: 305312
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(305312)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13236

Query Match      3.3%; Score 50.8; DB 6; Length 305312;
Best Local Similarity 57.6%; Pred. No. 0.071;
Matches 91; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Cy 1369 ATCTACCTCCGATTTGATTTGATTAATTTATTCATGCTTTATTTATTTATTTATTTA 1428
Db 140893 ATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 140834

Cy 1429 CTAAATTTATTCATGCAATTTATGAGCTAATGTTATTTATTTATTTATTTATTTGA 1468
Db 140833 TTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 140774

Cy 1489 AATGTGTTTATGATTTATCAATTAATTTGCAATTTAGTTTAA 1526
Db 140773 TATTTATTTATTTATTTATTTATTTATTTATTTATTTA 140736

RESULT 2
US-11-121-086-30/C
; Sequence 30, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
```

APPLICANT: POULSEN, TIM S.  
APPLICANT: NIELSEN, KIRSTEN V.  
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
FILE REFERENCE: 09138, 6000-00000  
CURRENT APPLICATION NUMBER: US/11/121,086  
CURRENT FILING DATE: 2005-05-04  
PRIORITY APPLICATION NUMBER: 60/567,570  
PRIORITY FILING DATE: 2004-05-04  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 30  
LENGTH: 158692  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-121-086-30

Query Match 2.9%; Score 45.2; DB 7; Length 158692;  
Best Local Similarity 56.8%; Pred. No. 1.3;  
Matches 83; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1383 TTGATTCATATATTCATCATGTTTATATTTTATTAATTTTACTAAATTTACATGA 1442  
DB 154813 TGTGATTTATATTTGCTATTTATGTTTATCTGAAATATTAATGCACTTTATTCATCA 154754  
QY 1443 CAATTTAGGACTAGTACTTATTTATGTTTATATTTGAATGCTTTTAAGT 1502  
DB 154753 AAAATTCATTAACCAATTAATTTTAAATATTCCTTCCTTAAGCATTTGTATTAAGT 154694  
QY 1503 TACATAAATTCGCAATTAGTTTAAA 1528  
DB 154693 TCATTAATAAATAATTAATGAATA 154688

RESULT 3  
US-10-995-561-13303/C  
Sequence 13303, Application US/10995561  
Publication No. US20050272054A1  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
FILE REFERENCE: CL001559  
CURRENT APPLICATION NUMBER: US/10/995,561  
CURRENT FILING DATE: 2004-11-24  
NUMBER OF SEQ ID NOS: 85702  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13303  
LENGTH: 201990  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(201990)  
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
US-10-995-561-13303

Query Match 2.9%; Score 45; DB 6; Length 201990;  
Best Local Similarity 56.4%; Pred. No. 1.7;  
Matches 84; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1389 TGATATATTTTCATCATGTTTATATTTTATTAATTTTACTAAATTTACATGACAACTT 1448  
DB 78616 TAAATATTTATATATTTTATATATTTTATATATTTTATATATATATATATATATTTTA 78557  
QY 1449 ATGGAGTAAGTACTTATTTATGTTTATATTTGAATGCTTTTAAGTTACATA 1508  
DB 78556 TTTTATATATTTATATATTTTATATATATATATATATATATATATATATATATTTTAA 78497  
QY 1509 AAATGCAATTAGTTTAAAAA 1537  
DB 78496 TATTTCTGCTCTCTGTTGAGGGGAAAAA 78468

RESULT 4  
US-10-995-561-13314/C  
Sequence 13314, Application US/10995561  
Publication No. US20050272054A1  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
FILE REFERENCE: CL001559  
CURRENT APPLICATION NUMBER: US/10/995,561  
CURRENT FILING DATE: 2004-11-24  
NUMBER OF SEQ ID NOS: 85702  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13314  
LENGTH: 119036  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(119036)  
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
US-10-995-561-13314

Query Match 2.9%; Score 44.6; DB 6; Length 119036;  
Best Local Similarity 55.5%; Pred. No. 1.6;  
Matches 86; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1383 TTGATTCATATATTCATCATGTTTATATTTTATTAATTTTACTAAATTTACATGA 1442  
DB 31696 TTATATATATATATATATTTTATATATTTTATATATATTTTATATATATATATATCA 31637  
QY 1443 CAATTTAGGACTAGTACTTATTTATGTTTATATTTGAATGCTTTTAAGT 1502  
DB 31636 TATTTATATATATATATATTTTATATATTTTATATATATTTTATATATATATATCT 31577  
QY 1503 TACATAAATTCGCAATTAGTTTAAAAA 1537  
DB 31576 TATTTATATATATTTTAT 31542

RESULT 5  
US-11-121-086-25/C  
Sequence 25, Application US/11121086  
Publication No. US20050266459A1  
GENERAL INFORMATION:  
APPLICANT: POULSEN, TIM S.  
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
FILE REFERENCE: 09138, 6000-00000  
CURRENT APPLICATION NUMBER: US/11/121,086  
CURRENT FILING DATE: 2005-05-04  
PRIORITY APPLICATION NUMBER: 60/567,570  
PRIORITY FILING DATE: 2004-05-04  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 25  
LENGTH: 173602  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-121-086-25

Query Match 2.8%; Score 43.8; DB 7; Length 173602;  
Best Local Similarity 55.6%; Pred. No. 3.3;  
Matches 84; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 1387 ATGGATATATTTTCATCATGTTTATATTTTATTAATTTTACTAAATTTACATGACAACT 1446  
DB 136252 ATTATATATATATATATATTTTATATATTTTATATATATATATATATATATATATAT 136193  
QY 1447 TTATGGAGTAAGTACTTATTTATGTTTATATATTTTGAATGCTTTTAAGTTACA 1506

Dd 136132 ATATATAATATTTTATTATATCTATATAAATATATATTTATTTATATATTTTA 136133

Dy 1507 TAAATTCGAATTAGTTTTAAAAAAA 1537  
||||| - ||||| - ||||| - |||||  
Db 136132 TAAATATATTAATATATTTTATATATAAAAA 136102

## RESULT 6

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1 Sequence 1 Application US/11155492
2 Publication No. US20050286479A1
3 GENERAL INFORMATION:
4 APPLICANT: Weissenbach, Jean
5 APPLICANT: Hazan, Jamil
6 TITLE OF INVENTION: CLONING, EXPRESSION AND CHARACTERIZATION OF THE SPG4
7 TITLE OF INVENTION: GENE RESPONSIBLE FOR THE MOST COMMON FORM OF AUTOSOMAL
8 TITLE OF INVENTION: DOMINANT SPASTIC PARAPLEGIA
9 FILE REFERENCE: R-341894
10 CURRENT APPLICATION NUMBER: US/11/155,492
11 PRIOR FILING DATE: 2005-06-20
12 PRIOR APPLICATION NUMBER: US/09/830,902
13 PRIOR FILING DATE: 2001-05-02
14 PRIOR APPLICATION NUMBER: FR 99 11097
15 PRIOR FILING DATE: 1999-09-03
16 PRIOR APPLICATION NUMBER: PCT/FR00/02433
17 PRIOR FILING DATE: 2000-09-04
18 NUMBER OF SEQ ID NOS: 107
19 SOFTWARE: PatentIn Vers. 2.0
20 SEQ ID NO 1
21 LENGTH: 110000
22 TYPE: DNA
23 ORGANISM: Homo sapiens
24 FEATURE:
25 NAME/KEY: exon
26 LOCATION: (9932) ... (10471)
27 FEATURE:
28 NAME/KEY: intron
29 LOCATION: (10472) ... (33718)
30 FEATURE:
31 NAME/KEY: exon
32 LOCATION: (33719) ... (33805)
33 FEATURE:
34 NAME/KEY: intron
35 LOCATION: (33806) ... (35748)
36 FEATURE:
37 NAME/KEY: exon
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55 NAME/KEY: exon
56 LOCATION: (61928) ... (62061)
57 FEATURE:
58 NAME/KEY: intron
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60 FEATURE:
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62 LOCATION: (62345) ... (62438)
63 FEATURE:
64 NAME/KEY: intron

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LOCATION:	(62439) ... (73173)
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LOCATION:	(89562) ... (89641)
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NAME/KEY:	intnon
LOCATION:	(89642) ... (91162)
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NAME/KEY:	exon
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NAME/KEY:	intnon
LOCATION:	(91234) ... (93443)
FEATURE:	
NAME/KEY:	exon
LOCATION:	(93444) ... (93484)
FEATURE:	
NAME/KEY:	intnon
LOCATION:	(93485) ... (100539)
FEATURE:	
NAME/KEY:	exon
LOCATION:	(100600) ... (102009)
JS-11-155-492-1	

Query Match	2.8%	Score 43.6;	DB 7;	Length 110000;
Best Local Similarity	56.2%	Pred. No. 2.8;		
Matches	82;	Conservative	0;	Mismatches 64;
			Indels	0;
			Gaps	0;

QY	1392	TATATATTCATCATGTTTAAATTTTAAATTTTCTAAATTTATGACATTAATG	1451
Db	107003	TATATATTCCTCAATATATTAACATTTATGCGCTCTGACCCCTCATGATATTCTGT	1069444
QY	1452	GGACTAGTACTCTTTATATATGTTATATATTTGAAATGTTTTAAATTCATATAAA	1511
Db	106943	CTATATTTTACTTACATATATATATATTAACACCTGCATATCTATTTTGTGTGCTTAAA	1068848
QY	1512	TTGCAATTAGTTTAAAAAATAAA	1537





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Oy      1383  TTGGATTGATTAATTAATTCATCAAGTTTAAATTTTATATAAATTTTCTAATAATTACATGA 1442
Db      1580  TTTTATTATTAAGGCTCAATAATTTTCTATAATTAATTATATAGTACGTTACTGC 1649
Oy      1443  CAATTATGAGCACTAAGTTACTTATTTATATATGTTTATATATATTTGGAATGTGTTTAAGT 1502
Db      1650  TAAATAAATTAATCTCATTTTGATATCCAAATCTGTGTCCTATATGATTCCTTCTTAGT 1709
Oy      1503  TACA 1506
Db      1710  AAAA 1713

RESULT 11
US-11-121-086-25
: Sequence 25, Application US/11121086
: Publication No. US20050266459A1
: GENERAL INFORMATION:
: APPLICANT: POULSEN, TIM S.
: APPLICANT: NIELSEN, KRISTEN V.
: TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
: FILE REFERENCE: 09138, 6000-00000
: CURRENT APPLICATION NUMBER: US/11/121, 086
: CURRENT FILING DATE: 2005-05-04
: PRIOR APPLICATION NUMBER: 60/567, 570
: PRIOR FILING DATE: 2004-05-04
: NUMBER OF SEQ ID NOS: 107
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 25
: LENGTH: 173602
: TYPE: DNA
: ORGANISM: Homo sapiens
US-11-121-086-25

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[illegible]

;	TYPE:	DNA	13866881301738
;	ORGANISM:	Bovine	
US-10-750-185-64246			
Query Match	2.7%;	Score 42;	DB 6;
Best Local Similarity	51.6%;	Pred. No. 0.62;	Length 1659;
Matches 96;	Conservative 0;	Mismatches 90;	Indels 0;
		Gaps 0;	
QY	1351	TGGCTCCTCTGAGGAAGATCTACCTCCGTAATTGATGTAAATATTTCATCATGTTT	1410
Db	1559	TGAATATTTCATTAACAAACAATTTTACTAGTCATATAAGAGAACATATTATATGAAATTAA	1500
QY	1411	ATATTTTATTAATTTTACTAAATTTACATGACAACTTATGGGACTAAGTACTATTATTA	1470
Db	1499	TTTTTTTTTAAATTTTGGCAAGGATTTATGCAAAATTAATAATACTCAAGCCGTAATCTT	1440
QY	1471	TATGTTATTAATATTGGAATGCTTTTAAGTACATATAAATGCAATTAGTTTAAATA	1530
Db	1439	TATAGCTAATTTCTCGATTTTATTTTAATTTACATATAATACAAATATCAATCTTTAAACATA	1380
QY	1531	AAAAAA	1536
Db	1379	CACATA	1374

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RESULT 13
US-10-750-185-46813
; Sequence 46813, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46813
; LENGTH: 4063
; TYPE: DNA
; ORGANISM: Bovine 1986688102899
US-10-750-185-46813

Query Match 2.7%; Score 41.8; DB 6; Length 4063;
Best Local Similarity 55.0%; Pred.No.1.2;
Matches 82; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 1382 ATTGATTTGTAATTAATTTTCATCAAGTTTATATTTTATATAAATTTTACTAATTTACATG 1441
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2389 ATTGGATCAATATAATAATGTCATTTAATTTTATACACATGTAACAAATTAATTTGTAAT 2448

Qy 1442 ACAATTTATGGGACTAAGTACTATTATTATATATGTTTATATATATTGAAATGCTTTTAA 1501
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2449 CTATGATGATCTCTATTATAGCTATGATCTGTAAAGTATATATACAAAGAGATCTTGTTTATA 2508

Qy 1502 TTACATTAATAATTCGATTTAGTTTAAAAA 1530
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2509 TTGCATACAAATTTTAAAAACAAGTTTTTAAA 2537

RESULT 14
US-10-995-561-13235
; Sequence 13235, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: December 26, 2005, 08:04:27 ; Search time 1348.14 Seconds  
(without alignments)  
9427.811 Million cell updates/sec

Title: US-10-674-540A-1

Perfect score: 1537

Sequence: 1 gcacgagccattcccaaac.....ctagttcaaaaaaaaaa 1537

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_NA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1537	100.0	1537	US-10-674-540-1	Sequence 1, Appli
2	448	29.1	1900	US-10-424-599-10323	Sequence 10323, A
3	351.4	22.9	1239	US-09-938-842A-2482	Sequence 2482, Ap
4	351.4	22.9	1239	US-09-938-842A-2482	Sequence 2482, Ap
5	291.2	18.9	1167	US-10-674-540-15	Sequence 15, Appl
6	165.6	10.8	2199	US-10-437-963-60348	Sequence 60348, A
7	154	10.0	1340	US-10-437-963-911	Sequence 911, App
8	152.4	9.9	778	US-10-767-701-23	Sequence 23, Appl
9	151	9.8	1384	US-10-425-114-31427	Sequence 31427, A
10	151	9.8	1384	US-10-425-114-31427	Sequence 31427, A
11	139.4	9.1	786	US-10-425-115-55840	Sequence 55840, A
12	133	8.7	464	US-10-767-701-28008	Sequence 28008, A
13	131.8	8.6	923	US-10-674-540-6	Sequence 6, Appli
14	124.6	8.1	588	US-10-424-599-43547	Sequence 43547, A
15	117.6	7.7	1481	US-10-437-963-13102	Sequence 13102, A
16	112.6	7.3	1481	US-10-425-115-21097	Sequence 21097, A
17	110.4	7.2	1812	US-10-437-963-47718	Sequence 47718, A
18	109.6	7.1	594	US-10-260-238-5250	Sequence 5250, Ap
19	107.4	7.0	2812	US-10-437-963-36187	Sequence 36187, A
20	105.6	6.9	2043	US-10-425-114-32590	Sequence 32590, A
21	105.6	6.9	2138	US-10-425-115-159545	Sequence 159545, A
22	104.6	6.8	1543	US-10-437-963-36545	Sequence 36545, A
23	101.4	6.6	1417	US-10-739-930-506	Sequence 506, App

C-24	98.4	6.4	1589	US-10-739-930-4239	Sequence 4239, Ap
C-25	98.2	6.4	2812	US-10-437-963-36187	Sequence 36187, A
26	97	6.3	1257	US-10-437-963-50552	Sequence 50552, A
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29	92	6.0	1522	US-10-425-114-15537	Sequence 15537, A
30	92	6.0	2008	US-10-425-114-17036	Sequence 17036, A
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36	90.2	5.9	688	US-10-767-701-7110	Sequence 7110, Ap
37	88.2	5.7	640	US-10-767-701-4765	Sequence 4765, Ap
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39	85.4	5.6	1627	US-10-425-114-10902	Sequence 10902, A
40	85.4	5.6	1784	US-10-424-599-12392	Sequence 12392, A
41	79	5.1	552	US-10-437-963-36185	Sequence 36185, A
42	77	5.0	1518	US-10-425-114-4612	Sequence 4612, Ap
43	76.8	5.0	1641	US-10-425-114-10888	Sequence 10888, A
44	75.8	4.9	2014	US-10-424-599-48229	Sequence 48229, A
45	72.2	4.7	900	US-10-425-115-14816	Sequence 14816, A

#### ALIGNMENTS

RESULT 1  
US-10-674-540-1  
Sequence 1, Application US/10674540  
Publication No. US20040158891A1  
GENERAL INFORMATION:  
APPLICANT: John E. THOMPSON et al.  
TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE.  
TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN PLANTS  
FILE REFERENCE: 10799-10  
CURRENT APPLICATION NUMBER: US/10/674, 540  
CURRENT FILING DATE: 2003-10-01  
PRIOR APPLICATION NUMBER: 09/597, 774  
PRIOR FILING DATE: 2000-06-09  
PRIOR APPLICATION NUMBER: 09/250, 280  
PRIOR FILING DATE: 1999-02-16  
PRIOR APPLICATION NUMBER: 09/105, 815  
PRIOR FILING DATE: 1998-06-26  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1537  
TYPE: DNA  
ORGANISM: Plant  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (48) ... (1390)  
US-10-674-540-1  
Query Match 100.0%; Score 1537; DB 7; Length 1537;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1537; Conserved 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 2  
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; Sequence 10323, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ. ID NOS: 285684  
; SEQ. ID NO 10323  
; LENGTH: 1900  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_109323C.1  
US-10-424-599-10323

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QY 1519 TAGTTTTTAA 1528  
DB 1786 TTATGTTTAA 1795

RESULT 3  
US-09-938-842A-2482  
; Sequence 2482, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 2482  
; LENGTH: 1239  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-2482  
Query Match 22.9%; Score 351.4; DB 3; Length 1239;  
Best Local Similarity 57.9%; Pred. No. 8.8e-73;  
Matches 752; Conservative 0; Mismatches 466; Indels 81; Gaps 4;  
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DB 135 CTTGTCACAGCAACCAAACTCAAGTACTGTGAGCGCAGCGCTACGCAAAATCTTCTT 194  
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DB 252 CGCCAGCTCGTGTCTCTCTCCGAAAGTTGTCTTCCATCAATCAATCAAGATTC 311  
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DB 312 TTGGGACCGTGAAGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 371  
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DB 372 GGTCTTGAAGCGCGTGAAGATTAATGATGATGATGATGATGATGATGATGATGATG 431  
QY 509 GGTGATGTTCTTGGGCTCAAGCTGAGTCACTGATGATGATGATGATGATGATGATGAT 568  
DB 432 GGTCAATGTTTGGGTCTAGGCACTTCAAGCTGAGCTTCTGCTGAGCCGAGCA 491  
QY 569 TACTCATGTTGAAAGGTGAAATGAGAAAGAAAGAGATTCATTAATCAAGTTGTA 628  
DB 492 GAATGTTCTGGGTGTAGTTGA-----GTA 520  
QY 629 CGACTGTTTCAATATCAACTTACTAGTTCGGGTCCAAAGCAAGAAAGAGAGCGA 688  
DB 521 CGACTTT-----GATATGA 536  
QY 689 CGACGAGATGATGACGACCCCAAGTATGATGATGATGATGATGATGATGATGATGATG 748

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Db      537 CAGTGAAGATGAGAGAGGTGTAAAGTGTACTCGGGGTGCTCACAATCTTACTCTCAA 596
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RESULT 4
US-09-938-842A-2482
; Sequence 2482, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2482
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

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US-09-938-842A-2482
Query Match      22.9%; Score 351.4; DB 3; Length 1239;
Best Local Similarity 57.9%; Pred. No. 8.8e-73;
Matches 752; Conservative 0; Mismatches 466; Indels 81; Gaps 4;

Qy      89 CCGAATGAGCCCGAATCTCTCGGTCCTAATGCTTTGGGCGGGCTACTAAACCGCTCAA 148
Db      15 CACATCATGGGAAAGAACTCTTAGGCTCAAGAAATGGGACACTATCTTAACCATTAAGA 74
Qy      149 CGATGAGCTCCGAGAGCTCTCCAGCGTCGCGGGGACCTTCGACAGTGCATACGACAC 208
Db      75 CCAATCATTAAGGAACTCATCTTACCTTTGGGCACTTTTGTCAAGCCACTACGATGC 134
Qy      209 CTTCAATTAACGACAGAACTGTCCTACTGCGGACGACGCGCTACGGAAGCGGACCT 268
Db      135 CTTGCTCAAGCAACCAAACTTCAAGTACTGTGAGCGCAGCGGATCGGCAAACTTCTT 194
Qy      269 ACTTCATTAAGACCGCTTCCCGGGGGGCGACACGGTTTGAAGTGTGCGCTACTTGT 328
Db      195 CTTGCAAGAG---GTCAATGCTCGAAAACGCTTCGACTACGAGGTTGTAACTTCTCTA 251
Qy      329 CGCCACTGCGAAGGTACGCGTCCAGAGGGGTTTCTGCTGAAGTCAAGTCAAGGAGAA 388
Db      252 CGCCACAGCTGTGTCTCTCCGGAAGTTTGTCTTCAATCACAATCAAGAGATTC 311
Qy      389 GTGGATAGGGAATCGAATTTGATTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 448
Db      312 TTGGGACCGGTGAGTCTAATCTGTGTGCTACATTTGCTGACGTCGATGAAGGCTTAA 371
Qy      449 GTGGCGGAGCAAGAAAGGAGTGTATGTGTGTGAGAGGGACTTTTGGATTATGATG 508
Db      372 GGCCTTAGGACGCGGTGAGATCTATATAGCTTTGAGAGGAACGACGAGAACTATGATG 431
Qy      509 GCTTGATGCTCTTGTGCTCAACTGAGTGTGCTCATCTTTGTACGACTCAACAAC 568
Db      432 GGTCAATGTTTGTGTCTACGCACTTAAGCTGACCTTGTGACGACCGACCGACGA 491
Qy      569 TACTCATGTTGAAAAGGTGAAAATGAGAAAAGAAAGATTCATTAATCAAGTTGTA 628
Db      492 GGAATGTTCTGTGTGTGTATGTA-----GGTA 520
Qy      629 CGACTGTTTCATATTCAACTACTAGTCCGCGCTCCAAAGACAAAGAAAAGAAACGA 688
Db      521 GCACTTT-----GATATGTA 536
Qy      689 CGAGCAAGATATATGACGACCCCAAGATGATCAAGTTGATGCAATATACATCGGA 748
Db      537 CAGTGAAGATGAAGAAAGGTGTAAAGTGTGCTCGGGTGTCAAACTATATCTTAA 596
Qy      749 GGATCCCAATCACCCTTTCACAAAATCTAAGTGAAGAAACAACTTGAGACCAACTCAA 808
Db      597 TCACCCCGAATCGAAATTCACCTAAGCTGAGTCAAGCTCAAGTTTAAAGATCAA 656
Qy      809 ACACTAATGACAAATACAAAGAAGAAACCTTAAGCATTAATTCGCCGGTCAAGCCT 868
Db      657 GGAAGCTTCTGTGAAGTAAAGACGAGAAACCGAGATGTGTGACTGGAACATAGCTT 716
Qy      869 AGGCGGACACTATCAAGTCGTAGACGCGCTTCGACATAGTGAAGAA---TTCACGACCGA 925
Db      717 GGGAGCTACAGAGGCTGTTCGGCCGCTATGATATAGCTGAGAACGGTTCCAGTATGA 776
Qy      926 GATCCCACTCAGGCGCGGTCTTCGGGTGCCAAAGTGAAGCAACAAAATTCACA 985
Db      777 TGTTCGGTCACTGTATAGTCTTGTGTGTCACAGTGAAGAAAGAGTTCAAGGA 836
Qy      986 ACTCTTGACTGTACCAACCTTAATGTCTCTCATGTAAAGAAATGTCATGCACTGAT 1045
Db      837 CGAAGTATAGTACAAAGAACTTAAGATCTCTCATGTAAAGAAACGATTTGATCTT 896
Qy      1046 CCTCTGTATCCCGTGAATCTCATGAGTTACGTGAACATAGGAATCGAGCTGAGATGGA 1105
Db      897 AACTCGATACCAAGGGGACCTTTAGGGTATGTGACATAGGAATTAACCTTTGATCGA 956

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QY	1106	CTCAGGAAAGTCGACCTTTCTTAAAGAACTGAAAAAACCGAGTAGATTGGCATTAATTGGCA	1165
QY	957	TACAAAGAAAGTCACCGCTCTCTTAAGCGATTCAAGGATCAGGAGATGCGCATTAATCTTCA	1016
QY	1166	AGCAATATTGCATGTTGTAAAGTGTGGCATGCGGATTAAAGGGGAGTTTAAGTTGTAA	1225
Db	1017	GGCATTGTTACATGTTGTAGCTGATGAAATGGGAAGAAAGAGGTTTAACCTGATGCT	1076
QY	1226	TAAGAGAAGTTCGATCTGTTTAATTAATCAATGATTTTCTTAAGAAAGAAATGTTGCT	1285
Db	1077	TAAGAGAAGTATTGCATTAGTAGAACAAATCAATGCGAGTTCTTGAAGCTGAGTGTGGT	1136
QY	1286	TCTCCAGCTTGATGCGTTGTGCAGAACAAAGGATGCTTTTGAATAGATGCTGATG	1345
Db	1137	GCCAGGATCTTGGTGGGTAGAGAAAGAAACAAAGGACTGATCAAGAACGAATGCTGAATG	1196
QY	1346	GGTTTGGCTCTCTGAGGAAGATCCATCCTGGAAT	1384
Db	1197	GGTCTGTGCTCCGTTGAAGAAACCTGATCTGAAT	1235

## RESULT 5

```

US-10-674-540-15
: Sequence 15, Application US/10674540
: Publication No. US20040158891A1
: GENERAL INFORMATION:
: APPLICANT: John E. THOMPSON et al.
: TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
: TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
: TITLE OF INVENTION: PLANTS
: FILE REFERENCE: 10799-10
: CURRENT APPLICATION NUMBER: US/10/674,540
: CURRENT FILING DATE: 2003-10-01
: PRIOR APPLICATION NUMBER: 09/597,774
: PRIOR FILING DATE: 2000-06-09
: PRIOR APPLICATION NUMBER: 09/250,280
: PRIOR FILING DATE: 1999-02-16
: PRIOR APPLICATION NUMBER: 09/105,815
: PRIOR FILING DATE: 1998-06-26
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 15
: LENGTH: 1167
: TYPE: DNA
: ORGANISM: Plant
: FEATURES:
: NAME/KEY: CDS
: LOCATION: (1) ... (1044)
: US-10-674-540-15

```

Query Match	18.9%;	Score 291.2;	DB 7;	Length 1167;
Best Local Similarity	64.3%;	Pred. No. 1.8e-58;		
Matches 453;	Conservative	0;	Mismatches 248;	Indels 3;
				Gaps 1

Qy	684	GGCGACGACGACGATGATGACGACCCCAAGATGTCAGATGGTGGATGTCACATATACAC	743
Db	340	AGTGACAGTGAAGATGATGAAGAGGGTATTAAGGTGATCTCGGGTGGCTCACAAATCTATCT	359
Qy	744	TCGGAGATATCCCAATTCACCCCTTCACAAACTTAAGTGCAGAAACACACTTCAGACCAA	803
Db	400	TCTATATCACCCCGAATTCGAAATTCCTAAGCTGAGCTACGGTCAACAGTTGTTAGCCAA	459
Qy	804	CTCAAAACAATATGACAAATATACAAAGACGAACCCCTATAGCATTAATTCGCGGGTAC	863
Db	460	ATCAAGGAGCTTCTGTGGAAGTATTAAGACGAGAAACCGAGCATTTGTGTACTGACAT	519
Qy	864	AGCCTAAGGCGGACACACTATCACTCGGAGACGGCTTCGACATAGTGGAGAA---TTCACG	920
Db	520	AGCTTGGGACCTACAGAGGGCTGTTCTGGCCGGCTTATGATTAATCTAGAAACGGTTCCAGT	579
Qy	921	ACCGAGATCCCACTACGGCCGCTGTCTTCGGGTGCCCAAAAGTATGACACAAAAATTC	980

Db	580	GATGATGTTCCGGTCACCTGCAATAGTCTTTGGTTGTCCACAGGTAGGAAAACAAGAGTTC	639
Oy	981	CAACAACCTTTGCACTCGTATGCCAAACCTTAATGTCTCCATGTGAAGGATGTCAATGCAC	1040
Db	640	AGAGACGAAAGTAATGAGTCAACAAGACTTAAGAATCCCATGTGAAGGAACAGCATTTGAT	699
Oy	1041	CTGATCCCTCTGTAATCCCGTGAAACTCATGGGTTAAGTGAAATGAAATGAGAGTGGAG	1100
Db	700	CTTTAACTCGATACCAGGGGGACTTTTATGGGTATGTGGACATAGGAATTAACCTTTGTG	759
Oy	1101	ATGCACTCGAAGAAAGTGCACCTTTCTTAAGAAGCTCGAAAAACCGAGTGAATTTGGCATAT	1160
Db	760	ATCGATCAAAAGAAAGTCAACCTTCTTAAGCATTTCAAGGATCCAGGGGATTTGGCATAT	819
Oy	1161	TTTGCAGCAATATTCGATCTTTGTGAAGTGTGGCATGGGGTTAAGGGGACTTTAAGTT	1220
Db	820	CTTAGCGGAGATGATCAATGTTGTAGCTGAGATGGGAAGAAAGGAGATTTTAACTG	879
Oy	1221	GTAATAAGAGAGAGTGTGTTTTGTTTAATTAAGCATGTGATTTTCTTAAGGAAGAATGT	1280
Db	880	ATGTGTTAAGAAATATTCGATTAAGTAAACAAGTCATCGAGTCTTGAAGCTGAGTGT	939
Oy	1281	TTTGGTTCTCAGCTTGTTGGTGGTGTGCAGAAACAAGGAGTGTTTGAATTAAGATGGT	1340
Db	940	TTGTGTCCAGGATCTTGTGTGGTGTGAAGAAACAAGGACTGATCAAGAACGAAGATGGT	999
Oy	1341	GAGTGGGTTTTGGCTCTCCCTGAGGAAGATCTCACTCTTGAAATTT	1384
Db	1000	GAATGGGTTCTTGCTCCCGTTGAAGAAAGAACCTTACTCTGAATTT	1043

## RESULT 6

```

US-10-437-963-60348
; Sequence 60348, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 60348
; LENGTH: 2199
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530.61865C.1
US-10-437-963-60348

```

Query Match	10.8%;	Score 165.6;	DB 7;	Length 2199;
Best Local Similarity	54.5%;	Pred. No. 1.9e-28;		
Matches 367;	Conservative	0;	Mismatches 289;	Indels 18;
				Gaps 1;

Qy	714	GTATTCAGAGTTTGATGATGACAAATTATACCAATCGAGAGATCCCAAAATACCCCTTCACAAAA	773
Db	1189	GTCTATGAAGGGGGTGTATCTCATCTTAACAGCTCCACCGACGAGCGCTCCCTTTCTCCAAAG	1248
Qy	774	CTAAGTCAGAGAACACAACACTTCAGACCAAACTCAAAACAATATAGACAAATATACAAAGAC	833
Db	1249	TACAGCGCGCCGACACAGATGCTCGCGCCGTCGCGAGCTGTGGCCAGGTACACGGAAC	1308
Qy	834	GAAGCCCTTAAGCATTAACATTGGCCGGTCACAGCCTTAGCGCGGACACTATCAGTGGTAGGC	893
Db	1309	GAGAGCCTTCGGCGTCGTCTGTGACCGAGGACACGCTTCGGCGGGTGGCTTCCACAGCCTCTGCG	1368

Qy	894	GCCTTCGACATAGTGGAGAAATCTCAGACCCGAG-----ATGCCAGTGC	935
Db	1369	GCCTTCGATATGTGTCTCAACGGCGTGTCCAAAGTCCGCGACGCGCGACATCCCGGTG	1428
Qy	936	ACGGCGCGTGTCTTCGCGGTGCCCAAAGTAAAGCAGACAAATAATTCACAACACTCTTGAC	995
Db	1429	ACCGCGGTGTGTTCCGGAGCCCGCAGATCCGGAAACCCGGAATTCAGAAAGCAGTTCCGAG	1488
Qy	996	TCGTAACCCAAACCTAAATGTCTCTCATGTAAAGAAATGTCATGACCTGATCCCTGTAT	1055
Db	1489	GAGCAGCCCAACCTCGCGGGGGCTGCACGTCAAGAAACATGCCGACCTCATCCGCTTAC	1548
Qy	1056	CCCGTGAACCTCATGGGTTACGTGAACATAGGAATCGAGTGGAGATCGACTCGAGAAAG	1115
Db	1549	CCGAGCGGCTCTCTCCGCTACCGCAACGTCCGGAACAACTCCAGGTCGACTCCAAAG	1608
Qy	1116	TCGACCTTCTTAAGGACTCGAAAAACCGAGTGTGGCATATATTGCAAGCAATATTG	1175
Db	1609	TGCCCCCTACGTGAAGCGAAGCACACGACCGAGCGACTACCAACAACCTGCAGGGGATCCTA	1668
Qy	1176	CATGTTGTAAAGTGTGGCATGTGGGTTAAAGGGGAGTTTAAAGTTGTAATTAAGAGAAGT	1235
Db	1669	CACACGGTGGCCGCGCTGGAACGGGAAGACGGCGAATTCAGACTCCAGGTGAAGCGCAGC	1728
Qy	1236	GTTGCAATGGTTAATAATGATCATGTGATTTTCTTAAGGAAGAAATGTTGTTCTCCAGCT	1295
Db	1729	GTCCGGCTGTGTAACAAGTCGACGGCTTCTCAAGGACAGCAACTGTGCGGAGTCA	1788
Qy	1296	TGCTGGGTGTGTCAGAACAAAGGATGGTTTGTATTAAGATGATGTAGTGGTTTGGCT	1355
Db	1789	TGCTGGGTGTGAGGGAACAAAGCATGTGTGCTCGGCCAAGAACGGGGAATGGCACTCGAG	1848
Qy	1356	CCTCCGAGGAAGA	1369
Db	1849	GGGCCCCGACAGGA	1862

```

RESULT 7
US-10-437-963-911
; Sequence 911, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 911
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_100828C.1
US-10-437-963-911

```

Query Match	10.0%	Score 154	DB 7	Length 1340
Best Local Similarity	54.7%	Pred. No. 8, 2e-25		
Matches 374	Conservative 0	Mismatches 300	Indels 10	Gaps 3
QY	688	ACGACGACGATGATGACGACCCCAAGTATGCAAGTTGATATACATATACATCGG	747	
DB	429	AGGGCCAGCGAGTGATGACCTCTGTGTGATGGGGGGTGCTCTGTGTGACAC-GATG	487	

QY	748	AGAGATCCCAATCAACCCCTTCCAAAACTAAGTGCAGAAAGCAACAACTTCGACCAAACTCA	807
Db	488	CCGATCCAGAAATCTCAGTACAAATTAAGCAGAGTGCAGATATCAAGTCTTGAATAGATCA	547
QY	808	AACAATAATGACAAATAACAAAGACGAAACCTTAAGCAATACATTCGCGGTCAAGCC	867
Db	548	AACGGCTCCAGGATATGTATCGAGCATGAGAGATCAGCATCACTTAACAGGCCACAGCC	607
QY	868	TAGCGCGCAACTATCAATCGTGAAGCGCTTCGACATAGTGGAGAAATCTCAGACCGGAA	927
Db	608	TTGGGGCTGCACCTTGCACCAATCAATGCGCATGACATTTGCTCCAAATGGTTACAAAGAA	667
QY	928	TC---CCAGTACACGGCCGTGTCTTCGGGTGCCCCAAAGTAGGCAACAAAAATTCCAAC	984
Db	668	GCTGTCCAGTGTCTGTCCCTTCGTCTTCGGTAGGCCAAAGATGGGGCAACCGTATTTTCAAG	727
QY	985	AACCTTTCGACTCGTACCCAAACCTAAATGTCTCTCATGTAAAGAAATGTCAATCGACTGA	1044
Db	728	AAGCGTTTCGACAGTGTCTCCAGATTGTGAATTTGCTCCGCAATTCCTCTGTATGTGG	787
QY	1045	TCCCTCTGTATCCCGTGAAACATCAAGGGTAACTGTAACATAGAAATCGAGTGGAGATGG	1104
Db	788	TTCCAAACTGGCC-----AAAATAGATATACGCAATGTCTGGCACAGAGCTGATGATGG	841
QY	1105	ACTCGAGAGAGTGCACCTTTCTTAAAGAACTCGAAAAAACCAGATGATTTGGCATTAATTGCG	1164
Db	842	ATACAGGGAAGTCAACATACCTGAAGGGCCCTGGGAATCCCTTAACGTGGCATGACATGG	901
QY	1165	AAGCAATATTTGCATTTGTGAATGTGTGGCATGTGGGTTAAGGGGAGTTTAAGTTGTMA	1224
Db	902	AGTGTACATGTATGGGGGTTCGCCGGAACGCAAGGGAAGCAACGAGAGGTTCAAGCTGGAGA	961
QY	1225	ATTAAGAGAAGTGTTCATTTGGTTAATTAAGTCATGTGATTTTCTTAAGAGAAATGTTTGG	1284
Db	962	TTGATTCGAGACATTTCTTTGTTAACAAACAGGAACCCACATGGAAGATGTGATGCAA	1021
QY	1285	TTCTCCAGCTTGTGTGGGTGTGCAAGCAAAAGGATGTTTGAATTAAGATGCTGAGT	1344
Db	1022	TTCCATCGTCTTGTGGGTGTGCAAGCAAAAGATATGTGAAAGGACGAGATGTGCGGT	1081
QY	1345	GGGTTTGGCTCCTCTGAGGAG	1368
Db	1082	GGCATTTGGCCGACCATAGAGATG	1105

```

RESULT 8
US-10-767-701-23
; Sequence 23, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 23
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAAY03-CLUS100312_1
US-10-767-701-23

```

Query Match	9.9%	Score 152.4;	DB 7;	Length 778;
Best Local Similarity	57.5%;	Pred. No. 1.5e-25;		
Matches 323;	Conservative	0;	Mismatches 221;	Indels 18;
			Gaps	2;
QY	839	CCTAAGCATTAACATTGCGCGGTACAGCCTTAGCGCGGACACATATCAGTGTGAGGCCCTT	898	



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Db 9 CCTGAGCATCTGTGCAAGGGCCACAGCCCTCGGCGCTGCTGGCCACGCTCTGCGCCTT 68
Qy CGACATAGTGAAGATCTCAGA-----CGAGATCCCAAGTCAAGCGCCT 943
Db 69 CGACATGCGGTGAACGGCGGTGTCCAGGGTGGCGCGCCGACATCCCGTACGGCCAT 128
Qy 944 GGTCTTGGGTCGCCCAAAAGTAGGCAACAAAATTCCAAACAATCTTGACTGTAACC 1003
Db 129 GGTGTTCGGGAGCCCGCAGATCGGGAAACCGGAGTTCAAGAAAGATTTCAGAGAGCTGCC 188
Qy 1004 AAACCTTAATGTCTCTCACTGAAGATGATGATGACTGATCCCTCTGTATCCCGTGA 1063
Db 189 CAACCTGGGCGGTGCACTGCAAGAACCCCGACCTGATCCCGTGTACCCGAGCGG 248
Qy 1064 ACTGATGGGTAACTGTAACATAGGAATGAGTGAAGTGCAGTCCGAGAGAGTGAC--- 1120
Db 249 CTTCTTGGGCTTACGCAACGCGCGGAGCTCTGCGCTGTGACTCCAAAGAGTGGCGCTA 308
Qy 1121 CTTTCTTAAGGACTCGAAAACCCGAGTATTTGGCATATTTGCAAGCAATATTGCAATGT 1180
Db 309 CGTGAAGAAGACTCTCAACCACTCGGGGACTACCAACCTGCAAGGCACTCTGCAAC 368
Qy 1181 TGTAGTGTGTGCAATGGGGTTAAAGGGGAGTTTAAAGTTTAAATTAAGAAAGTGTTC 1240
Db 369 GGTGGCGGGCTGGAACGGCAAGACGGGAGTTCAAGCTGCAAGGTGCAAGCGCAGCTGGC 428
Qy 1241 ATTGGTAAATAGTCAATGTATTTCTTAAAGAAAGATTTGTTCTCTCAAGTGTGTG 1300
Db 429 GCTGTGAACAAAGTGTCTCGGCTTCTCAAGGACGACAACTCTGCGCGAGTCAATGTG 488
Qy 1301 GGTGTGCAAGAACAAAGGATGTTTGAATTAAGATGATGAGTGTGTTGGCTCTCC 1360
Db 489 GGTGAAGCGGAACAAAGGAGTGTGATCGAGAAACCGGAGTGTGGAGCTCGAGCTCC 548
Qy 1361 TGAGGAAGATCTTACTCTCTGA 1382
Db 549 TGCCGAGGAAGAACCTTCCCGTA 570

RESULT 9
US-10-425-114-31427
; Sequence 31427, Application US/10425114
; Publication No. US2004003488BA1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 31427
; LENGTH: 1384
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73170B05_FLI
US-10-425-114-31427
```

Query Match 9.8%; Score 151; DB 7; Length 1384;  
Best Local Similarity 53.8%; Pred. No. 4.3e-25;  
Matches 363; Conservative 0; Mismatches 300; Indels 12; Gaps 2;

```
Qy 702 GACGACCCCAAGATGATGCAAGTTGATGACATATATCAATGAGAGATCCCAATCA 761
Db 556 GCCAACCCCTGTGTGATGATGAGGGGTCTTCACTACAGAGTGTGCTGAGGGTCA 615
Qy 762 CCTTCACAAAATTAAGTGAAGAACAACTTGAGACCAAACTCAAACTAATATGCA 821
```

```
Db 616 CAGTACAAACAAAGAGACGGCAAGCATCAGTGTTAACAGAGGTGAAGATACAGAT 675
Qy 822 AAATACAAAGACGAACCCCTTAAGCATTAATCCCGGTGCAACCTTACGGCCACTA 881
Db 676 CTGTACAAGCCAGAGGAGACGAGCATCACTAAACAGCCCAACCTTACGAGAGCTT 735
Qy 882 TCAGTCGAGCGCTTTCAGATAGT-----GGAAGATCTCAAGCCGAGATCCCAATC 935
Db 736 GCCACATCAACGCAACCGACATCTCTCCAAAGGCTTCAACAGAGAGCTGTGCTGTG 795
Qy 936 ACGGCGGTGTCTTTCGGGTGCCAAAGTAGGCAACAAAATTCCAACAATCTTTCAG 995
Db 796 TCGGCTTCGATTCGGGAGCCCGAGAGTGGAAACCTTGATTTCCAGAAAGCGCTTGC 855
Qy 996 TCGTACCAAACTTAATGTCTTCATGTAAAGATGATGATCTGATCCCTCTGTAT 1055
Db 856 AGCGGCGGACCTGAGAGCTGCTCGGCTCGGAACTCTCCGACGTGTGCCAAATGG 915
Qy 1056 CCGGTAAACTCATGGGTAACTGTAACATAGGAATGAGTGCAGTGCAGTGCAGAGAG 1115
Db 916 CCAAG-----CTAGGTACAGTATGTGCGCACAGCTGATGATGACACAGAGAA 969
Qy 1116 TCGACCTTCTTAAAGACTCGAAAACCCGAGTATTTGGCATTAATTTGCAAGCAATATG 1175
Db 970 TCGCGTACCTGAAGGCCCCCGAAGACCCCTGACATGAGTACATGAGTGTGATCATG 1029
Qy 1176 CATGTGTAGTGTGTGATGAGTGTGATTAAGGGGAGTTTAAAGTTTAAATTAAGAAAGT 1235
Db 1030 CACGGGCTGCTGTGGGCTCAAGGGGAGCAGCGGAGGTTGCGTGTGTGATCGGGAC 1089
Qy 1236 GTTGCATTTGTTAATAGTCAATGTATTTCTTAAAGAAAGATTTGGTCTCTCAAGT 1295
Db 1090 GTTGTGTGTGAACAAAGCATGAAGATGCTTGAAATGATGTTGCTGCCACCGTGC 1149
Qy 1296 TGTGTGTGTGTGCAACAAAGGATGTTTGAATTAAGATGATGATGATGATGATGATG 1355
Db 1150 TGTGTGTGTGTGCAACAAAGGATGATGATGATGATGATGATGATGATGATGATGATG 1209
Qy 1356 CTTCTGAGGAAGT 1370
Db 1210 GACCATGAGGAGGAT 1224

RESULT 10
US-10-425-115-105259
; Sequence 105259, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 105259
; LENGTH: 1384
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_27497C.1
US-10-425-115-105259
```

Query Match 9.8%; Score 151; DB 8; Length 1384;  
Best Local Similarity 53.8%; Pred. No. 4.3e-25;  
Matches 363; Conservative 0; Mismatches 300; Indels 12; Gaps 2;

```
Qy 702 GACGACCCCAAGATGATGCAAGTTGATGACATATATCAATGAGAGATCCCAATCA 761
Db 556 GCCAACCCCTGTGTGATGATGAGGGGTCTTCACTACAGAGTGTGCTGAGGGTCA 615
Qy 762 CCTTCACAAAATTAAGTGAAGAACAACTTGAGACCAAACTCAAACTAATATGCA 821
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```

Db      556 GCCAACCCCTGTGTGATGAGAGGTGCTTTCACTTACACAGATGCTGATCCAGGGTCA 615
Qy      762 CCCCTTCAAAACCTAAGTGAAGAAACAACCTTCAAGCCAACTCAAACTAATATGACA 821
Db      616 CAGTACAAACAAAGAGCGCAAGACATAGGTGTTAAACGAGTGAAGAAAGGATTCAGGAT 675
Qy      822 AAATACAAAGACGAACCCCTAAGCATTAATTCGCGGTCAAGCTTAAGCGCGCACTA 881
Db      676 CTGTACAAAGCAGAGAGACAGATCACTAATACAGCCCAAGCTTAAGAGACACTT 735
Qy      882 TCACTGTAGCGCTTCTGACATAGT-----GGAAATCTCAAGACCGAATCCAGTC 935
Db      736 GCCACATCAACGCAACCGACATGCTCTCAACGCTCAACAGAGCTGCTGCTGTGT 795
Qy      936 AGCGCGGTGCTTCCGGTGGCCAAAGTAGCAACAAATTCACAACTCTTGAC 995
Db      796 TCCCGCTTGTATTCGGAGAGCCAGAGTCGAAACCTTGATTTCCAGAGCGCTTGAC 855
Qy      996 TCGTACCCAAACCTAATATGCTCTCATGTAAAGAAATGTCATGACCTGATCCCTGTAT 1055
Db      856 AGCGCGGCGACCTGAGGCTGCTCCGCTCCGAACTCCCGACGTGCTCCCAATGG 915
Qy      1056 CCCGTAAACTCATGAGGTACGTGAACATAGGAATCGAGCTGAGATGACTCGAGAG 1115
Db      916 CCAAG-----CTAGGGGTACAGTATGTCGCAAGAGCTGATGATGACACAGAGAA 969
Qy      1116 TCGACCTTTTAAAGGACTCGAAACCCGAGTATGAGCAATTTGCAAGCAATATTG 1175
Db      970 TCGCGTACCTGAAGGCCCCCTGGAACCCCTGACATGACATGAGTGTCTACATG 1029
Qy      1176 CATGTGTAGTGTGTCATGAGGTAAAGGGAGGAGTTAAAGTTGTAATTAAGAGAGT 1235
Db      1030 CACGGGTCGCTGGGGCTCAAGGGAGCAGCGAGGGTTGAGCTGTGTGATCGATCGGAC 1089
Qy      1236 GTTGCAATGTTAATAGTCACTGATTTTCTTAAGAAAGATGTTGCTCTCACT 1295
Db      1090 GTTCTGTGTGAACAAACATGAAGATGCTCTGAAGAAATGATTCGCTCCACCGTCG 1149
Qy      1296 TGTGTGGTGTGCAAGAAAGGAGTGTGTTGAATTAAGATGAGTGGGTTTGGCT 1355
Db      1150 TGTGTGGTGTGCAAGAAAGTATGTTGAAGGCAAGATGCGCGGTGACATCTGACC 1209
Qy      1356 CCTCCTGAAGAAGT 1370
Db      1210 GACCATGAGAGAGAT 1224

RESULT 11
US-10-425-115-55840
; Sequence 55840, Application US/10425115
; Publication No. US2004021472A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 55840
; LENGTH: 786
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_150920C.1
US-10-425-115-55840

Query Match          9.1%; Score 139.4; DB 8; Length 786;
Best Local Similarity 57.6%; Pred. No. 1.8e-22;
Matches 270; Conservative 0; Mismatches 196; Indels 3; Gaps 1;

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Qy      70 TAGGCTCTCAAAAGCCGCGCAACATGCGCGAATCTCTGAGTCCATGCTTGGCCG 129
Db      163 TCGCGCGCGCCAAAGGCTCCGCGCATGCGGAGCTGCTCGGCTCCGCGCATGGAGG 222
Qy      130 GGTACTTAACCCGCTCAAGATAGAGTCCGTAGCTCTCTCAAGCTTGGGGGACCTTCT 189
Db      223 GCTCTCTGATTCCTCTGACCTCAAGCTCCGCGCGCTCATCTGCTGTGGCGACCTCT 282
Qy      190 GCCAGGTGACATACGACCTTCAATAAAGCAGAACTGTCTTACTGCGGAGCAGCC 249
Db      283 GCCAGTACCTTACGATTCCTTCAACTCCAGCACCACTCCAAATGATCTGGAGCTGCC 342
Qy      250 GCTACGGAAAGCGGACCTTACTATTAAGCCGCTTCCGCGGAGCGCAGACCGTTTG 309
Db      343 GTATCTCAGATCCACGCTCTTGCGCCGACAGCTGTCCGCGCGCGCGACATCTT-- 400
Qy      310 AGTGTGGGTGACTTGTAGCCACTGCGAAGGTCAAGCTCCAGAGCGCTTCTGTGA 369
Db      401 -CCGCGCGGTGACTCTTACGCAACCTCCAGTCTGTCTCCAGCGGTATCATGTGT 459
Qy      370 AGTGAAGTGAAGGAGAGTGGGATAGGAAATCGAATTTGATGATGCTGTGCTGT 429
Db      460 TCTGCTCTCCGCGAGCGGTGAACAAAGATCCAACTGATGCTTACGCTCTCCGTGT 519
Qy      430 CGAATGACAGACGAGTCCGGTGGCGGACGAAGAGGTATGTGTGAGAGAGGA 489
Db      520 CCAAGACGCGCGCGCGCGCCAGCGGCGGACGCGCATCTAGTCTGCGCGCGGCA 579
Qy      490 CTGTAGGATTAATGATGAGTGTGATTTCTTGTGTCTCACTTGAATC 538
Db      580 CCATCCGAGCGTGGAGTGGTTGACGTGCTCAAGCCGAGCTGCTCTC 628

RESULT 12
US-10-767-701-28008
; Sequence 28008, Application US/10767701
; Publication No. US2004017268A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 28008
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 7534916
US-10-767-701-28008

Query Match          8.7%; Score 133; DB 7; Length 464;
Best Local Similarity 58.9%; Pred. No. 4.5e-21;
Matches 248; Conservative 0; Mismatches 170; Indels 3; Gaps 1;

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Db 223 GCTACTCAGAGTCCACGCTCTTCGCTCGACGCTGTTCCCGCGCCGAC--ATCT 279  
Qy 310 ACGTGTGGCTACTTGTAGCCCACTGGAGGTCAAGGTCCCAAGGCGTTTCTGCTGA 369  
Db 280 CCGCGCGCGGTACTCTTACCGACCTCCAGTGTCTCCGCGCGGCATCATGTGTGT 339  
Qy 370 AGTCGAGTCAAGGAGAGTGGATAGGAATCGAATTGGATTGGTATGTCTGTGTGT 429  
Db 340 TCTGCTCTCCCGGAGGCGGTGAGCAGAGTCCAACTGATCGCTCTGCTGTGT 399  
Qy 430 CGAATGACGAGACGATCGGTGGCGGACGAGGAGGTATGTGTGTGAGAGGGA 489  
Db 400 CCAAGGACGCGCGCGCGCGCCACGAGGCGCGCTCATCTGATGTGGCGCGCGCA 459  
Qy 490 C 490  
Db 460 C 460

## RESULT 13

US-10-674-540-6  
; Sequence 6, Application US/10674540  
; Publication No. US20040158891A1  
; GENERAL INFORMATION:  
; APPLICANT: John E. THOMPSON et al.  
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE.  
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN  
; FILE OF INVENTION: PLANTS  
; FILE REFERENCE: 10799-10  
; CURRENT APPLICATION NUMBER: US/10/674,540  
; PRIOR FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: 09/597,774  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: 09/250,280  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 09/105,815  
; PRIOR FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Paedseq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 923  
; TYPE: DNA  
; ORGANISM: Plant  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (6)...(512)  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: (513)...(843)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (844)...(921)  
US-10-674-540-6

Query Match 8.6%; Score 131.8; DB 7; Length 923;  
Best Local Similarity 58.2%; Pred. No. 1.3e-20;  
Matches 251; Conservative 0; Mismatches 177; Indels 3; Gaps 1;

Qy 666 AAAGCAAGAGAAAGAAAGCAAGCAAGATGATGACGACCCCAAGATGATCAAGGT 725  
Db 90 AACAAAGAAAGATGAGATGAGAGAGAGAGAGATGATGATGATGATGATGATG 149  
Qy 726 TGATGATCATATATACATCGAGAGATCCCAATCACTCTTCAAAATCTAAGTCAAG 785  
Db 150 TGGCTTAAGATCTAGCTCTCAAGTACCGAAGTGTCTTCAAGACCTAAGTCAAGA 209  
Qy 786 AACAACTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 845  
Db 210 GAACAACTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 269  
Qy 846 ATTAATTCGCGGTCAAGCTTGAAGCGCAAGCAATCATCTGATGAGCGCTTCAAGATA 905

Db 270 ATAACTTTACAGGCGCATAGTCTTGTGATGATCTTACCTGTTTACCTCATTTGATGTG 329  
Qy 906 GTGGAGAA---TCTCAGACCGAGATCCCATGACGCGCGGTCTTGGGTGCCAAA 962  
Db 330 GTTGAATATGATGTGCGCATGTTGATGATGATGATGATGATGATGATGATGATG 389  
Qy 963 GTAGCAACAAATAATTCACAACTCTTGAATCTGATGATGATGATGATGATGATGAT 1022  
Db 390 GTTGGATATAGGATTCATTAAGAAATCAAGAAATTCATTAAGAAATTCATTAAG 449  
Qy 1023 GTAAAGATGATCATGATCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCT 1082  
Db 450 GTTAAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 509  
Qy 1083 ATAGGATGCA 1093  
Db 510 TCAGTATGTA 520

## RESULT 14

US-10-424-599-43547  
; Sequence 43547, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; PRIOR FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 43547  
; LENGTH: 588  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_139321C.1  
US-10-424-599-43547

Query Match 8.1%; Score 124.6; DB 7; Length 588;  
Best Local Similarity 54.5%; Pred. No. 5.1e-19;  
Matches 272; Conservative 0; Mismatches 224; Indels 3; Gaps 1;

Qy 92 AACATGCGCGCACTCTCTGAGTCAATGCTTGGCGCGGCTACTAATCCGCTCAACGA 151  
Db 33 AAATGAGAGAGACCTCAGTGGCAGAGCACTGGAAAGTCTGCTAGATCCTTACAT 92  
Qy 152 TGAGTCCGTGAGCTCTCTTACGCTGCGGGACTTGGCAGGTGATATACACACTT 211  
Db 93 TGATCTTGGCGGTACATTAATACATATGACAACTTGTCTCAATATATATATGCTTT 152  
Qy 212 CATTAACGACGAGAACTCTCTACTGCGGACAGAGCGGCTAAGCGGAGCGGACTACT 271  
Db 153 CAACTCAAGAAAGATCAATCAAGTATGCGGCAACGCCATACCTTAAGAAATTTCTT 212  
Qy 272 TCATTAAGACCGCTTCCCGGCGGCG--CGCAGACCGGTGATGAGTGTGCGTACTTGT 328  
Db 213 TTCCAAAGTATGATTTGAAAAACGAAACCTTTCAAGTATGAGTGAAGATTTCTCTA 272  
Qy 329 CGGCACTGCGAAGTCAAGCTCCCAAGAGCGTTTCTGCTGAAGTCAAGTCAAGGAGAA 388  
Db 273 CGAACTTCCAAAGCCAGCAGCAGCAGAAAGGTTTCTGCTCAAGTCTTTTCAAGGACTC 332  
Qy 389 GTGGATTAAGGAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 448  
Db 333 GTGAGACGACCAATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 392  
Qy 449 GGTGGCGGACGAAAGGAGGTGATGTGTGTGAGAGGAGACTTGTAGGATTAATGATG 508  
Db 393 AGCGTTGGGAGAGGAGCATATGATGATGATGATGATGATGATGATGATGATGATG 452

QY 509 GGTGATGTTCTTGATGCTCACTGAGTCGTCACTCTGTTGTTACGACTCAACAAC 568  
DB 453 GGTAAAGATTTTCACTTCCATTGTGATCTTCCGCTGAGATTTTGTGTTGTTCTC 512  
QY 569 TACTCATGTTGAAAAAGTG 587  
DB 513 TGCTCAAGTCACCATGGG 531

## RESULT 15

US-10-437-963-13102/c  
; Sequence 13102, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Mu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 13102  
; LENGTH: 1481  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_19168C.1  
US-10-437-963-13102

Query Match 7.7%; Score 117.6; DB 7; Length 1481;

Best Local Similarity 53.1%; Pred. No. 3.9e-17;  
Matches 305; Conservative 0; Mismatches 254; Indels 15; Gaps 2;

QY 805 TCAACCACTAATGACAAATACAAAGAGAAACCTTAAGCATTAATTCGCGGTCA 864  
DB 802 TCAAGAGCTAATGACAAATACAAAGAGAGACGAGACCATCACTCGTCGCGCAT 743  
QY 865 GCCTAGGCGGCACTATCACTGAGCGCTTGAATAGTGAATCTCAAGACG 924  
DB 742 GCCTGAGCGCGCTGCGACCTCAACGCGCGGACATGCTTCAAGCGCTGAATC 683  
QY 925 AGAT-----CCAGTCAAGCGCGTGTCTTGGGTGCCAAGTAGGCAAAAA 975  
DB 682 AGCAGCGCGCTGCGCGCTCAAGGCGGTGCTTGGCTGCGCGCGGTGCGGACTCG 623  
QY 976 AATTCAACAACTCTTCACTGTAACCAAACTTAATGCTCTCAATGAAGAAATGCA 1035  
DB 622 GATTCAAGAACTCTTCAAGAGCTCCCGGCTTCCGCTCTCGCGCTGCAACTGCG 563  
QY 1036 TCGACCTATCCCTGTATCCCGTGAACCTAAGGTTACGTGAACATPAGGAATCGAGC 1095  
DB 562 CGGAGGTGTCGCAAGTACC-----GCCGATGAGGTACGCGGACGTGCGGTGAGC 509  
QY 1096 TGGAGATCGAATCGAGAAAGTCACTTTCTAAAGAACTCGAATAACCGAGTATTGAC 1155  
DB 508 TCCCGGTGACACGAGAGAGTGGCCGTACTCAAGTCCCGGAGAACACAGCGGTGGC 449  
QY 1156 ATAAATTGCAAGCAATATTGCAATGTTGAAGTGTGGCAGTGAAGGGGAGTTTA 1215  
DB 448 ACAGCTCGAGGTACATGCGAGCGGTGCGCGGAGGCAAGCGCGGTGCA 389  
QY 1216 AGTTGTAAATAGAAAGTGTGATGCTTAATAGTCAATGATTTTCTTAAGAAAG 1275  
DB 388 AGCTGAGGTGACCGGAGCGTGGCGCTGTGTGAACAAGATGTGAACGCGCTCAAGAGG 329

QY 1276 AATGTTGTTCTCTCCAGCTTGTGAGTTGCAAGAACAAAGGATGTTTGAATAG 1335  
DB 328 AGTACCACTGCCCGCTCGTGAAGCGTCAAGAGGACAAAGGCAATGTGAGGCGCGC 269  
QY 1336 ATGATGAGTGGTTTGGCTCTCTGAGGAGGA 1369  
DB 268 ATGGCCACTGAAAGTTGATGATTTACAGAGGAGA 235

Search completed: December 26, 2005, 17:04:09  
Job time : 1353.14 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2005, 07:53:18 ; Search time 291.822 Seconds  
(without alignments)  
9362.258 Million cell updates/sec

Title: US-10-674-540A-1  
Perfect score: 1537  
Sequence: 1 gcacgagccattcccaaac.....ttagtttaaaaaaaaaa 1537

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued\_Patents\_NA.\*  
2: /cgn2\_6/ptodata/1/ina/1\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/5\_COMB.seq:\*  
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5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PC/US\_COMB.seq:\*  
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8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1537	100.0	1537	3	US-09-610-104C-1
2	291.2	18.9	1167	3	US-09-610-104C-15
3	131.8	8.6	923	3	US-09-610-104C-6
4	62.6	4.1	1344	2	US-09-610-104C-18
5	60.6	3.9	7218	2	US-08-232-463-14
6	51	3.3	1141	3	US-09-806-708B-22
7	48.4	3.1	17612	3	US-09-949-016-15061
8	47.2	3.1	32392	3	US-09-662-254B-27
9	46.4	3.0	601	3	US-09-949-016-148614
10	46.4	3.0	67755	3	US-09-949-016-13703
11	46.2	3.0	1663	3	US-08-827-171B-1
12	45.8	3.0	1663	3	US-09-588-995A-88
13	45.8	3.0	1663	3	US-09-596-062-1
14	45.8	3.0	18651	3	US-09-949-002-592
15	45.8	3.0	18682	3	US-09-949-002-786
16	45.8	3.0	640681	3	US-09-790-988-1
17	45.8	3.0	21358	3	US-09-973-278-789
18	45.6	3.0	21676	3	US-09-973-278-792
19	45.6	2.9	40655	3	US-09-949-016-12032
20	45.2	2.9	40655	3	US-09-949-016-15919
21	44.8	2.9	601	3	US-09-949-016-23926
22	44.8	2.9	601	3	US-09-949-016-148613
23	44.8	2.9	100863	3	US-09-949-016-17031
24	44.8	2.9	100863	3	US-09-949-016-17031

C 25	44.6	2.9	55866	3	US-09-949-016-15129	Sequence 15129, A
C 26	44.4	2.9	421118	3	US-09-949-016-16297	Sequence 16297, A
C 27	44.2	2.9	601	3	US-09-949-016-132805	Sequence 132805, A
C 28	44.2	2.9	96878	3	US-09-949-016-12551	Sequence 12551, A
C 29	44.2	2.9	187169	3	US-09-949-016-12776	Sequence 12776, A
C 30	44.2	2.9	191569	3	US-09-949-016-15940	Sequence 15940, A
C 31	44	2.9	700	3	US-09-735-271-1038	Sequence 1038, Ap
C 32	44	2.9	12313	3	US-09-949-016-13248	Sequence 13248, A
C 33	44	2.9	13830	3	US-09-614-981-8	Sequence 8, Appl1
C 34	43.8	2.8	17612	3	US-09-949-016-15061	Sequence 15061, A
C 35	43.8	2.8	50000	3	US-09-662-254B-24	Sequence 24, Appl1
C 36	43.8	2.8	231129	3	US-09-949-016-16110	Sequence 16110, A
C 37	43.8	2.8	266293	3	US-09-949-016-11934	Sequence 11934, A
C 38	43.6	2.8	20674	3	US-09-641-638-651	Sequence 651, App
C 39	43.6	2.8	20674	3	US-10-170-097-651	Sequence 651, App
C 40	43.6	2.8	51835	3	US-09-949-016-17101	Sequence 17101, A
C 41	43.6	2.8	52032	3	US-09-949-016-11789	Sequence 11789, A
C 42	43.6	2.8	110000	3	US-09-830-902-1	Sequence 1, Appl1
C 43	43.4	2.8	1341	3	US-09-830-230A-572	Sequence 572, App
C 44	43.4	2.8	1410	3	US-09-830-230A-571	Sequence 571, App
C 45	43.4	2.8	32099	3	US-09-949-016-16562	Sequence 16562, A

#### ALIGNMENTS

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RESULT 1
US-09-610-104C-1
; Sequence 1, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE.
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
; PRIOR FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1537
; TYPE: DNA
; ORGANISM: Plant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (48) ... (1390)
US-09-610-104C-1
Query Match 100.0%; Score 1537; DB 3; Length 1537;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACGAGCCATTCCAAAGCTCTTACGACACTCAAACTATTTCACATGAGCTGCAGAG 60
Db 1 GCACGAGCCATTCCAAAGCTCTTACGACACTCAAACTATTTCACATGAGCTGCAGAG 60
QY 61 CCCAACCTTTAGGCTCTCAAGCCGCGCCCAACATGAGCTCTCGGATCAATG 120
Db 61 CCCAACCTTTAGGCTCTCAAGCCGCGCCCAACATGAGCTCTCGGATCAATG 120
QY 121 CTTGGGCGGGCTACTAAACCGCTCAACGATGAGCTCCGTGAGCTCTCTAGGCTGCG 180
Db 121 CTTGGGCGGGCTACTAAACCGCTCAACGATGAGCTCCGTGAGCTCTCTAGGCTGCG 180
QY 181 GGGACTTCTGCAGAGTACATGACGACCTTCAATTAACGACAGAACTGCTACTGCG 240
Db 181 GGGACTTCTGCAGAGTACATGACGACCTTCAATTAACGACAGAACTGCTACTGCG 240
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QY      1321 TGGTTTGAATAAGATGATGTAGTGCGGTTTTGGCTCCTCTGAGAAATCCTACTCCGTG   1380
Db      1321 TGCTTTGAAATAGAAGATGTGTAGTGCGGTTTTGGCTCCTCTGAGAAATCCTACTCCGTG   1380
QY      1381 AATTGATGTGTAATATATTCATCATGTTTTATTTATTAATAATTTTACTAATTTACAT   1440
Db      1381 AATTGATGTGTAATATATTCATCATGTTTTATTTATTTATTAATAATTTTACTAATTTACAT   1440
QY      1441 GACAATTTATGSGACTAAGTACTATTTATTAATGTTATTTATTTATTTGAAGTGTGTTTAA   1500
Db      1441 GACAATTTATGSGACTAAGTACTATTTATTAATGTTATTTATTTATTTGAAGTGTGTTTAA   1500
QY      1501 GTTACATTAATTTGCATTAAGTTTAAAAAAA    1537
Db      1501 GTTACATTAATTTGCATTAAGTTTAAAAAAA    1537

RESULT 2
US-09-610-104C-15
; Sequence 15, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Plant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1044)
US-09-610-104C-15

Query Match          18.9%; Score 291.2; DB 3; Length 1167;
Best Local Similarity 64.3%; Pred. No. 1.le-67;
Matches 453; Conservative 0; Mismatches 248; Indels 3; Gaps 1;

        684 AGCGACGACGATGATGACGACCCCAAGTAGTCGAAGTTGATGCAATATACACA 743
Db       340 AGTGACAGTGAAGATGAGAAAGGTGAAGTGATGCTCGGTGCTCAAAATCTATACT 399
QY       744 TCGGAGATCCCAATTCACCCCTTCACAAAACCTAAGTGCAGAACACAACTTCAGACAAA 803
Db       400 TCTAATCACCCCCGAATTCGAAATCTAAGCTGAGCTCAAGCTCAAGTGTGTAAGCCAAG 459
QY       804 CTCGAACAACCTAATGACAAATAATACAAAGAGCAAAACCCTAAGCATTAATTCGCCGGTAC 863
Db       460 ATCAAAGAGCTTCTGTGTAAGTATTAAGGAGCAAGAAACGACATTTGTGTGACTGACAT 519
QY       864 AGCTTAGGCGGACACTATCACTCGTAGCGCCTTCGACATAGTGGAGAA---TCTCAGC 920
Db       520 AGCTTAGGACCTCAKAGAGGCTGTTCTGGCGGCTATGATATATGCTGAGAACGGITCCAGT 579
QY       921 ACCGAGATCCAGTCAAGCGCGCTGTCTTGGGTGCCAAAAGTAGGCAACAAAATTC 980
Db       580 GATGATGTTCCGTCACCTGCTATAGTCTTTGGTGTGCCACAGTAGGAAACAAAGAGTTC 639
QY       981 CAACAACCTTGTGACTCGTACCAACCTTAATGTCTCATGTATGAAGATGCATCGAC 1040

```

Db	640	AGAGACGAAGTAATAGTGCACAAAGAACTTAAAGATCTCTCATGTATGAAGAACACGATTAAT	699
Qy	1041	CTGATCCCTCTGTATTCCTCGTAAATCACTAGGGTTACGTAAACATATAGAAATTCGAGCTGGAG	1100
Db	700	CTCTTAATCTCGATTACCTCAAGGGGACCTTTTATGGGTATGTGACATATAGAAATTAACCTTTGGT	759
Qy	1101	ATCGACTCGAGGAAAGTCGACCTTTCTTAAAGGACTCGAAAAACCCGATGATTTGGCATTAAT	1160
Db	760	ATCGATACAAAGAAAGTCACCGTTTCTTACGCGATTCAGGAATTCAGGGGATTTGGCATTAAT	819
Qy	1161	TTGCAAGCAATATTTCATCTTTGTAAAGTGGTGGCATAGGGGTTAAGGGAGATTTAAGTT	1220
Db	820	CTTCAGGGGATTTTACATGTTTACGTGGAATGGAATGGGAAGAAAGAAAGTTTAACCTG	879
Qy	1221	GTAAATTAAGAAAGTGTTCGATTGGTTAAATTAATCATGTGATTTTCTTAAGGAAGAATGT	1280
Db	880	ATGCTTAAGAGAAATGATTGCATTAGTAGAACAGTCAATCGAGATCTTTGAAGCTGAGTGT	939
Qy	1281	TTGGTTTCTCCAGCTTTGGTGGGTTGTGCAGAACAAAGGATGGTTTTGAATTAAGATGGT	1340
Db	940	TTGGTGCCAGGATCTTTGGTGGGTATGAGAAAGAACAAAGGACTATTCAAAGAACGAATGGT	999
Qy	1341	GAGTGGGTTTTGGCTCTCTCTGAGGAAAGATTCCTACTCTCGAATTT	1384
Db	1000	GAATGGTCTTCTGCTCCGCTTGAAGAAAGAACTGTATCTGAATTT	1043

```

RESULT 3
US-09-610-104C-6
; Sequence 6, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610.104C
; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
; LENGTH: 923
; TYPE: DNA
; ORGANISM: Plant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(512)
; NAME/KEY: Intron
; LOCATION: (513)...(843)
; NAME/KEY: CDS
; LOCATION: (844)...(921)
US-09-610-104C-6

Query Match      8.6%; Score 131.8; DB 3; Length 923;
Best Local Similarity 58.2%; Pred.No.5e-25;
Matches 251; Conservative 0; Mismatches 177; Indels 3; Gaps 1;

QY      AAAAGCAAAAGGAAAAGGAAGCGACGACGATGTATGCAGCCCCCAAAGTATGCAGAAGT   725
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      90 AACCAACAAGAACGATGAGGATGAGACGAGACGAGAGATGAATCTAATAATGTGGTGG  149

QY      TGGATGACAAATATTACATTCGAGAGATCCCAATATCACCTTGACAAAACTTAAGTGCAAGA   785
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      150 TGGCTTAAGATTAGTGCTCAAGTAACCCGAGAGTGTCTTTTCACGAGACTTAAGTGCAAGA   209

QY      ACACAACTTCAGACCAACCACTCAACCAATATGACAAAATTCAGAAAGACGAAAACCTTAAGC   845

```

[illegible]

```

US-09-610-104C-18
RESULT 4
; Sequence 18, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Plant
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)...(1344)
US-09-610-104C-18

```

	Query Match	Similarity	4.1%	Score 62.6	DB 3	Length 1344
	Best Local	Similarity	51.2%	Pred. No. 2e-06		
	Matches	146	Conservative	0	Mismatches 133	Indels 0
					Gaps	0
Qy	1070	GGGTTACGTGAACATAGGAATCGAGCTGGAGATCGACTCGAGAAAGTCGACCTTCTTAA				11225
Db	978	GTGTTATATAGCACCGTGGGGAGAGAGCTGGCGTTGGATCATCAGAACTCGCGTTTCTTAA				10333
Qy	1130	GGACTTCGAAAAACCCGAGTATTTGGCATTAATTGCCAAGCAATATTCGATGTTTGAAGG				11885
Db	1038	ACCTTCGGTGTATGTTTCTACTGCTCATTAATCTTGAAAGCTATGCTTCAATTACTTACGCG				10971
Qy	1190	TTGGCATGGGTTAAGGGGAGTTTAAAGTTGTAATATAGAAAGTGTTGCATTGGTTAA				12498
Db	1098	GTATCATGAAAAAGAGAGAGATTTTGCTGTGCAAGTGGGAGAGACCATGCGTAGTGA				11573
Qy	1250	TAAATCATATGATTTTCTTAAAGAAAGATTTTGGTTCCTCCAGCTGCTGAGTTGTGCA				13085
Db	1158	CAAGCGTCGACCTTTTGAAGAAGCATTTACAAATTCACCGTTTGGCTCAAGACGC				12171

Qy 1310 GAACAAGGATGTTTGAATAAGATGTGAGTGGTTTGGC 1354  
Db 1218 GAATTAAGATGTTTGGCAAGATGAAGTCTGTTGATTCACG 1262

## RESULT 5

US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-Fl8  
US-08-232-463-14

Query Match 3.9%; Score 60.6; DB 2; Length 7218;  
Best Local Similarity 3.1%; Pred. No. 1.6e-05;  
Matches 12; Conservative 227; Mismatches 146; Indels 0; Gaps 0;

Qy 371 GTCGAGTCGAGGAGGAGATGGAATGCAATTGGATGTCGTCGTC 430  
Db 1438 GTCGAGTCGAGGAGGAGATGGAATGCAATTGGATGTCGTCGTC 430  
Qy 431 GAATACAGACGATCGCGTCGCGGACGAAAGGAGGTATGCGTGGAGGAC 490  
Db 1378 GTCGAGTCGAGGAGGAGATGGAATGCAATTGGATGTCGTCGTC 430  
Qy 491 TTGAGGATTAAGTGGATGTTCTTGTCTCACTTGTCTCATCTTT 550  
Db 1318 GTCGAGTCGAGGAGGAGATGGAATGCAATTGGATGTCGTCGTC 430  
Qy 551 GTTACGACTCAACAACACTACTGTTGAAAGGTGAAATGAGAAAGACAT 610  
Db 1259 GTCGAGTCGAGGAGGAGATGGAATGCAATTGGATGTCGTCGTC 430  
Qy 610 GTTACGACTCAACAACACTACTGTTGAAAGGTGAAATGAGAAAGACAT 610  
Db 1199 GTTACGACTCAACAACACTACTGTTGAAAGGTGAAATGAGAAAGACAT 610

Qy 611 TCATTAATCAATGTTGATGACCTGTTCAATATCAACTACTGTCGCTCAAGA 670  
Db 1198 TCATTAATCAATGTTGATGACCTGTTCAATATCAACTACTGTCGCTCAAGA 670

Qy 671 CAAAGGAAAAGGAGGACGACGACGATGATGACGACCCCAAGTATGCAAGTTGAT 730  
Db 1138 CAAAGGAAAAGGAGGACGACGACGATGATGACGACCCCAAGTATGCAAGTTGAT 730

Qy 731 GACATATACATCGGAGGATCCC 755  
Db 1078 GACATATACATCGGAGGATCCC 755

## RESULT 6

US-09-806-708B-22  
Sequence 22, Application US/09806708B  
Patent No. 6784342  
GENERAL INFORMATION:  
APPLICANT: The University of British Columbia  
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants  
FILE REFERENCE: 4810-58741  
CURRENT APPLICATION NUMBER: US/09/806,708B  
CURRENT FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: US 60/147,133  
PRIOR FILING DATE: 1999-08-04  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 22  
LENGTH: 1141  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
NAME/KEY: promoter  
LOCATION: (1) (1141)  
OTHER INFORMATION: consensus sequence of A.c.t., L.a., and B.n. PAB1 promoters  
US-09-806-708B-22

Query Match 3.3%; Score 51; DB 3; Length 1141;  
Best Local Similarity 13.6%; Pred. No. 0.0024;  
Matches 103; Conservative 254; Mismatches 392; Indels 11; Gaps 2;

Qy 785 AACCAACTTCAGACCAACTCAAACTAATGACAAATACAAAGCAAACTTAAG 844  
Db 321 AACCAACTTCAGACCAACTCAAACTAATGACAAATACAAAGCAAACTTAAG 844  
Qy 845 CATTAACATTCGCGGTCACAGCCCTAGCGGACATCTCATGTCGCGCTTCGACAT 904  
Db 381 CATTAACATTCGCGGTCACAGCCCTAGCGGACATCTCATGTCGCGCTTCGACAT 904  
Qy 905 AGTGAAGATCTCAAGCCGATCCAGTCAAGCCGCTGCTTCGCGTCCCAAGT 964  
Db 441 AGTGAAGATCTCAAGCCGATCCAGTCAAGCCGCTGCTTCGCGTCCCAAGT 964  
Qy 965 AGGCAACAAAATTCACAACTTCGACCTGTCACCTCAAACTTAATGCTTCATGT 1024  
Db 501 AGGCAACAAAATTCACAACTTCGACCTGTCACCTCAAACTTAATGCTTCATGT 1024  
Qy 1025 AAGGAATGTCATGACCTGATCCCTGTATCCGCTAATCTCATGCGTTACGGAACAT 1084  
Db 561 AAGGAATGTCATGACCTGATCCCTGTATCCGCTAATCTCATGCGTTACGGAACAT 1084  
Qy 1085 AGAATGAGGTCGAGATGTCGACCTGGAAGTTCGACCTTCTTAAGACTGGAAGAAC 1144  
Db 621 AGAATGAGGTCGAGATGTCGACCTGGAAGTTCGACCTTCTTAAGACTGGAAGAAC 1144  
Qy 1145 GAGTATGAGGTCGATATTCGACCAATATGCAATGTTGTAAGTGGTGGCTTAA 1204  
Db 681 GAGTATGAGGTCGATATTCGACCAATATGCAATGTTGTAAGTGGTGGCTTAA 1204  
Qy 1205 GGGGAGTTTAAGGTTGTAATTAAGAGAAGTTCGATGTTGTAATTAAGTTCGATTT 1264  
Db 741 GGGGAGTTTAAGGTTGTAATTAAGAGAAGTTCGATGTTGTAATTAAGTTCGATTT 1264





```

Query Match      3.0%; Score 46.2; DB 3; Length 67755;
Best Local Similarity 56.1%; Pred. No. 0.35;
Matches 87; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Db
1382 ATTGATTGATAATTAATTTATTCATCATGTTTATTAATTTTATATAAATTTTACTAAATTTACATG 1441
ATTATAATATTTATTTATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 40963

1442 ACAATTATATGGACCTAGTACTTATATATATGTTTATTAATTTGAAGTGTTTAAG 1501
ATAATTATATATATATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 41023

1502 TTACATTAATAATTGCAATTAGTTTAAAAAATA 1536
TTATATTAATAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 41023

RESULT 12
US-08-827-171B-1
; Sequence 1, Application US/08827171B
; Patent No. 6254869
; GENERAL INFORMATION:
; APPLICANT: CAROLYN PETERSEN
; APPLICANT: JIN-XING HUANG
; TITLE OF INVENTION: CRYPTOPAIN VACCINES, ANTIBODIES, PROTEINS,
; TITLE OF INVENTION: PEPTIDES, DNA AND RNAs FOR PROPHYLAXIS,
; TITLE OF INVENTION: TREATMENT, DIAGNOSIS AND
; TITLE OF INVENTION: DETECTION OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIK A
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: California
; COUNTRY: United States of America
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
; COMPUTER: PC
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: Wordperfect 6.0a WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,171B
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/014,233
; FILING DATE: March 27, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hana Vermy
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: (HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-1677
; TELEFAX: (415) 324-1678
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1663 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: Cryptosporidium parvum
; US-08-827-171B-1

Query Match      3.0%; Score 45.8; DB 3; Length 1663;
Best Local Similarity 53.7%; Pred. No. 0.072;
Matches 77; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

1382 ATTGATTGATAATTAATTTATTCATCATGTTTATTAATTTTATATAAATTTTACTAAATTTACATG 1441
ATTATAATATTTATTTATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT

```

RESULT 14  
 US-09-598-062-1  
 : Sequence 1, Application US/09598062  
 : Patent No. 6759044  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: CAROLYN PETERSEN  
 :  
 : JIN-XING HUANG  
 :  
 : TITLE OF INVENTION:  
 : PEPTIDES, DUA AND RNAs FOR PROPHYLAXIS,  
 : TREATMENT, DIAGNOSIS AND  
 : DETECTION OF  
 :  
 : NUMBER OF SEQUENCES: 16  
 :  
 : CORRESPONDENCE ADDRESS:  
 :  
 : ADDRESSEE: PETERS, VERNY, JONES & BIK A

```

RESULT 15
US-09-949-002-592/c
: Sequence 592, Application US/09949002
: Patent No. 6900016
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: CL000790
: CURRENT APPLICATION NUMBER: US/09/949,002
: PRIOR APPLICATION NUMBER: 2000-01-28
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ. ID NOS: 10823
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 552
: LENGTH: 18651

```



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2005, 02:34:17 ; Search time 980.564 Seconds  
(without alignments)  
10446.670 Million cell updates/sec

Title: US-10-674-540A-1

Perfect score: 1537  
Sequence: 1 gccacgagccctcccaaac.....tagtttataaaaaaaaaa 1537

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: N\_Geneseq\_21:\*  
2: geneseqn1980s:\*  
3: geneseqn1990s:\*  
4: geneseqn2000s:\*  
5: geneseqn2001as:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1535.4	99.9	1537	3	AAAS3880 Senescenc
2	1535.4	99.9	1537	6	AAAS20751 CDNA enco
3	1535.4	22.9	1239	6	ABZ14677 Arabidops
4	351.4	22.9	1239	13	ADU20461 A. thalia
5	351.4	22.9	1239	13	ADU20618 A. thalia
6	351.4	22.9	1259	3	AAAC42410 Arabidops
7	291.2	18.9	1167	3	AAAS3885 Arabidops
8	291.2	18.9	1167	6	AAAS20756 Arabidops
9	169.4	11.0	1077	11	AC126423 Rice abio
10	165.6	10.8	1533	8	ADA71310 Rice gene
11	165.6	10.8	2064	8	ADA71310 Rice gene
12	151	9.8	1384	13	ADK60584 Plant ful
13	131.8	8.6	923	3	AAAS3884 Senescenc
14	131.8	8.6	923	6	AAAS20753 Partia1 g
15	111.6	7.3	1353	8	ADA69968 Rice gene
16	109.6	7.1	594	12	ADJ44250 Plant CDN
17	105.6	6.9	2043	13	ADK61747 Plant ful
18	104.6	6.8	1197	8	ADA69856 Rice gene
19	101.4	6.6	1396	3	AAAC41939 Arabidops

20	101.4	6.6	1398	3	AAAC41529 Arabidops
21	101.4	6.6	1400	3	AAAC40763 Arabidops
22	101.4	6.6	1417	13	ADT15180 Plant CDN
23	98.4	6.4	1589	13	ADT18913 Plant CDN
24	93	6.1	1576	13	ADK48466 Plant ful
25	92	6.0	1522	13	ADK32777 Plant ful
26	92	6.0	2008	13	ADK34216 Plant ful
27	91	5.9	1591	13	ADK3756 Plant ful
28	90.4	5.9	1878	13	ADK48110 Plant ful
29	90.4	5.9	1927	13	ADK32745 Plant ful
30	86.4	5.6	1164	8	ADA69718 Rice gene
31	85.4	5.6	1536	13	ADK28155 Plant ful
32	85.4	5.6	1627	13	ADK28082 Plant ful
33	81.2	5.3	6777	11	AC132126 Rice abio
34	77.4	5.0	240	10	AC131758 Rice abio
35	77.7	5.0	1518	13	ADK10037 Plant ful
36	76.8	5.0	1641	13	ADK28068 Plant ful
37	71.6	4.7	1507	13	ADK50603 Plant ful
38	65.4	4.3	229	12	ADJ10834 Recombina
39	65.2	4.2	779	10	ADL18245 Barley ge
40	62.6	4.1	636	13	ADK2858 Plant ful
41	62.6	4.1	1344	6	ABZ13508 Arabidops
42	62.6	4.1	1344	6	AAAS20757 CDNA enco
43	62.6	4.1	1344	8	ADA67881 Arabidops
44	62.6	4.1	1758	3	AAAC48392 Arabidops
45	62.6	4.1	1760	3	AAAC39568 Arabidops

ALIGNMENTS

RESULT 1	AAAS3880	standard; CDNA; 1537 BP.
ID	AAAS3880	
AC	AAAS3880	
DT	03-JAN-2001	(first entry)
DE	Senescence-induced lipase coding sequence.	
KW	Senescence-induced lipase; senescence; lipase; antisense; regulation; modulation; resistance; stress; crop protection; ethylene; ds.	
XX	Dianthus caryophyllus.	
OS		
FT	Key	Location/Qualifiers
FT	CDS	47..1391
FT		/*tag= a
FT		/product= "Senescence-induced lipase"
XX	MO200049164-A1.	
PD	24-AUG-2000.	
XX		
PP	14-FEB-2000; 2000MO-US003494.	
XX		
PR	16-FEB-1999; 99US-00250280.	
XX		
PA	(SENE-) SENESCO INC.	
XX		
PI	Thompson JB, Wang T, Hudak K, Hong Y;	
XX		
DR	WPI; 2000-549277/50.	
XX	P-PSDB; AAY97298.	
PT	DNA encoding carnation senescence-induced lipase, useful for regulating	
FT	the expression of senescence in plants to delay its onset and improve	
XX	plant resistance to environmental stress, thus extending shelf-life or	
PS	growth period.	
XX	Claim 1; Page 70; 89pp; English.	

CC insertion of the senescence-induced lipase coding sequence in an  
 CC antisense direction in a plant genome can be used to regulate the  
 CC expression of senescence in those plants. Alteration of expression of the  
 CC senescence-induced lipase gene in plants results in delayed onset of  
 CC senescence and improved resistance to environmental stresses, thus  
 CC extending the plant shelf-life and/or growth period. The genetically  
 CC altered plant is useful for producing a new variety or line of plants  
 CC where the alteration is stably transmitted from generation to generation.  
 CC This method of regulation is advantageous over prior senescence  
 CC modulating technologies since prior methods were only applicable to a  
 CC limited range of plants, e.g. to plants that are ethylene-sensitive. The  
 CC antisense regulation method is applicable to all types of plants,  
 CC regardless of ethylene sensitivity

XX Sequence 1537 BP; 448 A; 329 C; 381 G; 379 T; 0 U; 0 Other;

Query Match 99.9%; Score 1535.4; DB 3; Length 1537;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1536; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 GCACGAGCATTTCCAAAACCTCTTACACCACTCAAAATATTTCACATGCGTGCAGAG 60
DB 1 GCACGAGCATTTCCAAAACCTCTTACACCACTCAAAATATTTCACATGCGTGCAGAG 60
QY 61 CCCAACCTTTAGGCTCTCAAAAGCCGGCCCAACATGCGCCGAACTCCTCGGGTCCAAATG 120
DB 61 CCCAACCTTTAGGCTCTCAAAAGCCGGCCCAACATGCGCCGAACTCCTCGGGTCCAAATG 120
QY 121 CTTGGGCGGGCTATAAACCCTGCAAGATGAGCTCCGTGAGCTCCTCTGAGCTGGC 180
DB 121 CTTGGGCGGGCTATAAACCCTGCAAGATGAGCTCCGTGAGCTCCTCTGAGCTGGC 180
QY 181 GGGAGCTTCTGCAGGTGACATACGACACCTTATTAAGACCAAGATCGTCTAATCTGCG 240
DB 181 GGGAGCTTCTGCAGGTGACATACGACACCTTATTAAGACCAAGATCGTCTAATCTGCG 240
QY 241 GCACGAGCGCGCTACCGGAAGGCGGACCTTACTTATTAAGACCGCTTCCCGGGGGCGAG 300
DB 241 GCACGAGCGCGCTACCGGAAGGCGGACCTTACTTATTAAGACCGCTTCCCGGGGGCGAG 300
QY 301 ACCGGTTGACGTGGTGGCGTACTTGTACGCCACTGCGAAGGTCAAGCTCCAGAGGCGT 360
DB 301 ACCGGTTGACGTGGTGGCGTACTTGTACGCCACTGCGAAGGTCAAGCTCCAGAGGCGT 360
QY 361 TTCTGCTAAGTCCGAGGTGAGGGAAGTGGGAATCGAATTGGATTTGGGTATG 420
DB 361 TTCTGCTAAGTCCGAGGTGAGGGAAGTGGGAATCGAATTGGATTTGGGTATG 420
QY 421 TCGTGGTGTGCAATGACGAGACGAGTCCGGGTGGCGGACGAAGGATGTGTGTGT 480
DB 421 TCGTGGTGTGCAATGACGAGACGAGTCCGGGTGGCGGACGAAGGATGTGTGTGT 480
QY 481 GGAGAGGAGCTTGTAGGAGATTATGAGTGGGTGATGTTCTTGGTCTCAACTTGAAGTGTG 540
DB 481 GGAGAGGAGCTTGTAGGAGATTATGAGTGGGTGATGTTCTTGGTCTCAACTTGAAGTGTG 540
QY 541 CTCACTCTTTTGTGACGACTCAACAACTACTCATGTTGAAAAGGTGAAAATGAGAAA 600
DB 541 CTCACTCTTTTGTGACGACTCAACAACTACTCATGTTGAAAAGGTGAAAATGAGAAA 600
QY 601 AGAAGAGCATTCATTAATCAAGTTGTGAGTGTGCACTGTTCAATATCAACCTACTAGGTTCCG 660
DB 601 AGAAGAGCATTCATTAATCAAGTTGTGAGTGTGCACTGTTCAATATCAACCTACTAGGTTCCG 660
QY 661 CGTCCAAAGACAAAGAAAAGGAAGGACGACGACGATGATGACGACCCCAAAAGTATGTC 720
DB 661 CGTCCAAAGACAAAGAAAAGGAAGGACGACGACGATGATGACGACCCCAAAAGTATGTC 720
QY 721 AAGGTGATGACAAATATACATCGAGAGATCCCAAAATCACCTTCACAAAAATCTAAGTG 780
DB 721 AAGGTGATGACAAATATACATCGAGAGATCCCAAAATCACCTTCACAAAAATCTAAGTG 780
QY 781 CAAGAACAACACTTGAGACCAAACTCAACAACTAATGACAAATATCAAAAGACGAAGCC 840
  
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DB 781 CAAGAACAACACTTGAGACCAAACTCAACAACTAATGACAAATATCAAAAGACGAAGCC 840
QY 841 TTAAGCATTAACATTTGCGCGGTCAACAGCCTTAGCGGACACTATCAGTGTGAGCGCTTTCG 900
DB 841 TTAAGCATTAACATTTGCGCGGTCAACAGCCTTAGCGGACACTATCAGTGTGAGCGCTTTCG 900
QY 901 ACATATGAGGAATCTGACGACCGAGATCCAGTCCAGCGCGGTGTCTTGGGTGCCCA 960
DB 901 ACATATGAGGAATCTGACGACCGAGATCCAGTCCAGCGCGGTGTCTTGGGTGCCCA 960
QY 961 AAGTAGGCAACAAAATTTTCCAACTCTTCACTGCTGACCTGACCTCAAACTTAAATGCTCC 1020
DB 961 AAGTAGGCAACAAAATTTTCCAACTCTTCACTGCTGACCTGACCTCAAACTTAAATGCTCC 1020
QY 1021 ATGTAAGGAATGTCATGACCTGATCCCTCTGTATCCCGTAAACTATGAGGTTACGTGA 1080
DB 1021 ATGTAAGGAATGTCATGACCTGATCCCTCTGTATCCCGTAAACTATGAGGTTACGTGA 1080
QY 1081 ACATAGGAATCGAGCTGAGATCGACTCGAAGAACTGACCTTCTTAAAGGACTCGAAAA 1140
DB 1081 ACATAGGAATCGAGCTGAGATCGACTCGAAGAACTGACCTTCTTAAAGGACTCGAAAA 1140
QY 1141 ACCGAGTATGTCATTAATTTGCAACAAATTTGCAATTTGTTTGAAGTGTGGATGGGG 1200
DB 1141 ACCGAGTATGTCATTAATTTGCAACAAATTTGCAATTTGTTTGAAGTGTGGATGGGG 1200
QY 1201 TTAAGGGGAGTTTAAAGTTGTAAATTAAGAAAGTGTGATGTTGTTAAATTAAGTATGTG 1260
DB 1201 TTAAGGGGAGTTTAAAGTTGTAAATTAAGAAAGTGTGATGTTGTTAAATTAAGTATGTG 1260
QY 1261 ATTTCTTAAAGAAATGTTTGTCTCCAGCTTGTGGGTGTGCAAGAAAGGGA 1320
DB 1261 ATTTCTTAAAGAAATGTTTGTCTCCAGCTTGTGGGTGTGCAAGAAAGGGA 1320
QY 1321 TGTGTTTGAATTAAGATGAGTGTGTTTGGTCTCTCTGAGAAAGATCTTCTCTG 1380
DB 1321 TGTGTTTGAATTAAGATGAGTGTGTTTGGTCTCTCTGAGAAAGATCTTCTCTG 1380
QY 1381 AATTGATGATTAATTTTCACTGTTTATATTTTATATTTTACTTAAATTTTACAT 1440
DB 1381 AATTGATGATTAATTTTCACTGTTTATATTTTATATTTTACTTAAATTTTACAT 1440
QY 1441 GACAATTTATGAGGACTAAGTACTTATTAATGTTTATTAATTTGAAATGTTTAA 1500
DB 1441 GACAATTTATGAGGACTAAGTACTTATTAATGTTTATTAATTTGAAATGTTTAA 1500
QY 1501 GTTACATTAATTTGCAATTTGTTTAAAAA 1537
DB 1501 GTTACATTAATTTGCAATTTGTTTAAAAA 1537
  
```

RESULT 2  
 AAS20751  
 ID AAS20751 standard; cDNA; 1537 BP.  
 XX  
 AC AAS20751;  
 DT 09-APR-2002 (first entry)  
 XX  
 DE cDNA encoding carnation senescence-induced lipase.  
 XX  
 KW Plant; senescence-induced lipase; regulation of senescence;  
 KW environmental stress; carnation; gene; ss.  
 OS Dianthus caryophyllus.  
 XX  
 FH Key location/Qualifiers  
 FT CDS 48..1391  
 FT /\*tag= a  
 FT /product= "Senescence-induced lipase"  
 FT /transl\_except= (pos:255..257, aa:Glu)  
 XX

PN WO200198510-A2.  
 XX 27-DEC-2001.  
 XX 19-JUN-2001; 2001WO-US019385.  
 XX 19-JUN-2000; 2000US-00597774.  
 PR 05-JUL-2000; 2000US-00610104.  
 XX (SENSE-) SENESCO TECHNOLOGIES INC.  
 PA Thompson JE, Wang T, Hudak K, Hong Y;  
 PI WPI: 2002-1130793/17.  
 DR P-PSDB; AAU11997.  
 XX New carnation and Arabidopsis genes encoding a senescence-induced lipase,  
 PT useful for controlling (onset of) senescence in plants, regulating  
 PT expression of senescence in plants, or modifying senescence in transgenic  
 PT plants.  
 XX Claim 2, Fig 7, 106pp; English.  
 XX The present invention relates to the isolation of polynucleotide  
 CC sequences encoding plant (carnation and Arabidopsis) senescence-induced  
 CC lipases. Regulation of expression of senescence in plants is obtained by  
 CC integration of a gene or gene fragment encoding senescence-induced lipase  
 CC into the plant genome. The isolated polynucleotide sequences are useful  
 CC for controlling senescence or the onset of senescence in plants caused by  
 CC either internal or external factors (e.g. environmental stress), or  
 CC regulating expression of senescence in plants. The DNAs are also useful  
 CC for modifying senescence in transgenic plants. The present sequence  
 CC encodes for carnation senescence-induced lipase  
 CC  
 SQ Sequence 1537 BP; 448 A; 329 C; 381 G; 379 T; 0 U; 0 Other;  
 Query Match 99.9%; Score 1535.4; DB 6; Length 1537;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1536; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 481 GGAGAGGAGCTTGTAGGATTTATGAGGTGATGTTCTTGTGGTCTCACTTGAAGTCTG 540  
 Qy 541 CTCATCTCTTTGTATGAGATCTCAACAACTACTCATGTTGAAAGGTGAAATGAGAAA 600  
 Db 541 CTCATCTCTTTGTATGAGATCTCAACAACTACTCATGTTGAAAGGTGAAATGAGAAA 600  
 Qy 601 AGAAGACATTTCAATTAATCAAGTTGTAGCACTGTTTCAATATCAACTACTAGTTCG 660  
 Db 601 AGAAGACATTTCAATTAATCAAGTTGTAGCACTGTTTCAATATCAACTACTAGTTCG 660  
 Qy 661 CGTCCAAAGCAAAAGAAAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
 Db 661 CGTCCAAAGCAAAAGAAAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
 Qy 721 AAGGTTGATGACAAATATACATTCGAGAGATCCCAATACCTTCAAAAATTAAGT 780  
 Db 721 AAGGTTGATGACAAATATACATTCGAGAGATCCCAATACCTTCAAAAATTAAGT 780  
 Qy 781 CAAGACACAACTTCAAGCCAACTCAAACTCAATGACAAATACAAATACAAAGACCA 840  
 Db 781 CAAGACACAACTTCAAGCCAACTCAAACTCAATGACAAATACAAATACAAAGACCA 840  
 Qy 841 TAAACATTAATTCGCGGTTCACAGCCTAGCGGAGACATATCAGTGTAGCGCTTCG 900  
 Db 841 TAAACATTAATTCGCGGTTCACAGCCTAGCGGAGACATATCAGTGTAGCGCTTCG 900  
 Qy 901 ACATATGAGAGATCTCAACGACCGAGATCCAGTACAGCGGTGCTTGGGGTCCCA 960  
 Db 901 ACATATGAGAGATCTCAACGACCGAGATCCAGTACAGCGGTGCTTGGGGTCCCA 960  
 Qy 961 AAGTAGGCAACAAATTAATTCACAACTTTCGACTGATCCCAACCTAAATGCTCC 1020  
 Db 961 AAGTAGGCAACAAATTAATTCACAACTTTCGACTGATCCCAACCTAAATGCTCC 1020  
 Qy 1021 ATGTAAAGAAATGTCATGACCTGATCCCTGTATCCCGTAAATCATGAGTTACGTGA 1080  
 Db 1021 ATGTAAAGAAATGTCATGACCTGATCCCTGTATCCCGTAAATCATGAGTTACGTGA 1080  
 Qy 1081 ACATAGGAATGACCTGAGATGACATCGAGAGAGTGAACCTTTCTAAAGATCGAAAA 1140  
 Db 1081 ACATAGGAATGACCTGAGATGACATCGAGAGAGTGAACCTTTCTAAAGATCGAAAA 1140  
 Qy 1141 ACCGAGATGATGACATTAATTTGCAAGCAATATTCGATGTTGATGAGTGGATGGG 1200  
 Db 1141 ACCGAGATGATGACATTAATTTGCAAGCAATATTCGATGTTGATGAGTGGATGGG 1200  
 Qy 1201 TTAAGGGGAGTTTAAAGTTGTAATTAAGAGAGTGTGCAATGTTAATAGTCATGTG 1260  
 Db 1201 TTAAGGGGAGTTTAAAGTTGTAATTAAGAGAGTGTGCAATGTTAATAGTCATGTG 1260  
 Qy 1261 ATTTCTTAAAGAGAAATGTTGGTCTCCAGCTGTGTTGAGTGTGTCAGAAACAAAGGGA 1320  
 Db 1261 ATTTCTTAAAGAGAAATGTTGGTCTCCAGCTGTGTTGAGTGTGTCAGAAACAAAGGGA 1320  
 Qy 1321 TGGTTTGAATTAAGAGAGTGAAGTGGTGGTCTCCCTCGAAGAGATCTACTCTG 1380  
 Db 1321 TGGTTTGAATTAAGAGAGTGAAGTGGTGGTCTCCCTCGAAGAGATCTACTCTG 1380  
 Qy 1381 AATTGATGATTAATTAATTTCAATGTTTATATTTATTTATTTAATTTAATTTTACAT 1440  
 Db 1381 AATTGATGATTAATTAATTTCAATGTTTATATTTATTTAATTTAATTTTACAT 1440  
 Qy 1441 GACAATTTATGAGCTAAGTTACTTAATTTATATTTATTTATTTATTTATTTATTTAA 1500  
 Db 1441 GACAATTTATGAGCTAAGTTACTTAATTTATATTTATTTATTTATTTATTTATTTAA 1500  
 Qy 1501 GTTACATTAATTTGCAATTTGTTTAAAAAAA 1537  
 Db 1501 GTTACATTAATTTGCAATTTGTTTAAAAAAA 1537

RESULT 3

AB214677  
ID AB214677 standard; DNA; 1239 BP.  
XX  
AC AB214677;  
XX  
DT 21-JAN-2003 (first entry)  
XX  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2482.  
XX  
KM Arabidopsis thaliana; plant; gene; stress; transgenic; de.  
XX  
OS Arabidopsis thaliana.  
XX  
PN W0200216655-A2.  
XX  
PD 28-FEB-2002.  
XX  
PE 24-AUG-2001; 2001WO-US026685.  
XX  
PR 24-AUG-2000; 2000US-0227866P.  
PR 26-JAN-2001; 2001US-0264647P.  
PR 22-JUN-2001; 2001US-0300111P.  
XX  
PA (SCRI ) SCRIPPS RES INST.  
XX  
PI (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Harper JF, Krepe J, Wang X, Zhu T;  
XX  
DR WPI; 2002-304127/34.  
XX  
PT Identifying a stress condition to which a plant cell has been exposed and  
PT producing plants with increased tolerance to these abiotic stresses.  
XX  
XX Claim 144; SEQ ID NO 2482; 577bp + Sequence Listing; English.  
XX  
PS The invention relates to identifying a stress condition to which a plant  
CC cell has been exposed, comprising: (a) contacting nucleic acid  
CC representative of expressed polynucleotides in the plant cell with an  
CC array or probes representative of the plant cell genome; and (b)  
CC detecting a profile of expressed polynucleotides in the plant cell  
CC characteristic of a stress response. The method is useful in the  
CC production of transgenic plants, cells and seeds and in producing plants  
CC with increased tolerance to abiotic stresses. The present sequence is that  
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used  
CC in methods of the invention. Note: The sequence data for this patent is  
CC not represented in the printed specification but is based on sequence  
CC information supplied to Derwent by the European Patent Office  
XX  
SQ Sequence 1239 BP; 346 A; 249 C; 323 G; 321 T; 0 U; 0 Other;  
Query Match 22.9%; Score 351.4; DB 6; Length 1239;  
Beeb Local Similarity 57.9%; Pred. No. 3.7e-73;  
Matches 752; Conservative 0; Mismatches 466; Indels 81; Gaps 4;  
QY 89 CCCAACAAGGCCCGCAACTCTCGGGTCCCAATGCTTGGGCGGCTACTAAACCGCTCAA 148  
DB 15 CACATCATGGGAAGAACTCTTAGGCTCAAGAAATTGGACACTATCTTAGACCCATTGA 74  
QY 149 CGATGAGCTCCGTGAGCTCTCTCAAGCTGCGGGGACTTGTGCGAGTGAACATGACAC 208  
DB 75 CCAATCACTTAGGGAAGCACTTATGCTTGTGGGCACTTTGTCAAGCACTTAGATGC 134  
QY 209 CTTTCAATAAGCAACGAAGTCTCTACTGCGGCAAGCGGCTTACGGGAAGCGGACCT 268  
DB 135 CTTGCTCAACGACCAAACTCCCAAGTACTGTGAGCCAGCCGCTACGGCAATCTTCTTT 194  
QY 269 ACTTCATAAGACCGGCTTCCGGGGGGGCGACAGCGGTTGACGCGTGGGTACTTGA 328  
DB 195 CTTGCAACAAG--GTCATGCTGGAAGAAAGCTTCCAGCTACGAGGTTGTAATCTTCTTA 251  
QY 329 GCGCACTGCGAAGTCCAGAGCGGTTTCTGCTGAAGTCAAGTCCAGAGGAGAA 388  
DB 252 GCGCAGACTCGTGTCTTCTCTCCGGAAGGTTGCTTCTCCATCATCAATCAAGAGATTTC 311

QY 389 GTGGGATAGGAAATCGAATTGGAATTGGGTAATGTCGTGTGCAATGACGAGACTCG 448  
DB 312 TTGGGACCGTGAAGTCTAACTGGTTGGCTACATGCTGTCAAGCTATGAACCGTCTAA 371  
QY 449 GGTGGCGGAGCAAGGAGGTGTAATGTGTGTGAGAGGGAATTTGATGATTAATGATG 508  
DB 372 GGCCTTATGAGACGCGGTGAGATCTATAATGCTTTGAGAGGAACGAGCGAACTATGATG 431  
QY 509 GGTGATGTTCTTGGGTGCTCAACTGAGTGTGCTCATCTTGTGTAAGCACTCAACAAC 568  
DB 432 GGTCAATGTTTGGGTCTAGGCACTTACGCTGACCCCTTGTGCAAGGACCCGAGCA 491  
QY 569 TACTCATGTTGAAAAGGTGAAAATGAGAAAAGAGGACATTCATTAATCAAGTTGTA 628  
DB 492 GGATGTTCTGTGTGTATGTGA-----GTA 520  
QY 629 CGACTGTTTCAATATCAACTACTAGGTTCCGCTCCAAAGACAAAGAAAAGAGACGA 688  
DB 521 CGACTTTT-----GATATGA 536  
QY 689 CGACGAGATGATGACGACCCCAAGATGACAAAGTTGATGACAAATATACATGCGA 748  
DB 537 CAGTGAAGATGAAAGAGGTGTAAGTGAATGCTCGGTGCTCAAACTCTATCTTCTAA 596  
QY 749 GGAATCCCAATCAACCTTTCAAAAATAGTGCAGAAACAACCTTGACGACCAACTCAA 808  
DB 597 TCACCCGGAATCGAATTCATCTAAGTCAAGTCAAGTCAAGTGTATGCAAGATCAA 656  
QY 809 ACAACTAATGCAAAATATCAAAAGCAAAACCTTAAGATTAATCTCCCGGTCAACCT 868  
DB 657 GGAAGCTTGTGTAAGTATGAAGCAAGAAACCGAGCATTTGTGTGACTGGAACATTA 716  
QY 869 AGGCGCAACTATCAATCTGAGCGGCTTCGACATGTGAGAA---TTCACGACCGA 925  
DB 717 GGGAGCTACAGAGGCTGTTCGCGGCTATGATATGCTGAGAACGGTTCACATATGA 776  
QY 926 GATCCCAAGTCAACGCGCTGTGCTTCGGGTGCCCAAAATAGGCAACAAAATTCACA 985  
DB 777 TGTTCGGGTCACTGCTATAGCTTTGTTGTGTCACAGGTGAGAAACAAGAGTTCA 836  
QY 986 ACTCTGCACTGACCCAAACCTTAATGCTTCATGATGAAGAAATGTCATGACTGAT 1045  
DB 837 CGAAGTATGATGACAAAGAACTTAAGATCTTCATGTAAGGAACAGATGATCTCTT 896  
QY 1046 CCTCTGTATCCGTGAACCTCATGAGTTACGTGAACATGAGATTCAGCTGAGATCGA 1105  
DB 897 AACTCGATACCCAGGGGACTTTAAGGTATGTGACATGAGAAATTAATTTGATCGA 956  
QY 1106 CTGAGGAAAGTCAACTTTCTTAAGACTCGAAAAACCCGAGTATGGCATTAATTTGCA 1165  
DB 957 TACAAAGATGACACCTTCTTACAGATTCAGAGAAATCCAGGGATTTGCAATCTTCA 1016  
QY 1166 AGCAATATGCAATGTTGAATGTTGATGAGGATTAAGGGGAGTTTAAGTTGTA 1225  
DB 1017 GGCATGTTATCATGTTGATGATGATGAATGGAAGAAAGAGATTAACTGATGAT 1076  
QY 1226 TAAAGAAATGTTGATTTGTTAATAGTCAATGATTTTCTTAAGAAAGAAATGTTGCT 1285  
DB 1077 TAAAGAAATGTTGATTTGTTAATAGTCAATGATTTTCTTAAGAAAGTGTGTTGGT 1136  
QY 1286 TCTCCAGCTTGGGGTGTGCAAGAAAGAGGATGTTTGAATTAAGATGATGATG 1345  
DB 1137 GCGCAGATCTTGGGTGATGAGAAAGAAACAAAGGACTGATCAAGAAAGAAAGTGTGATG 1196  
QY 1346 GGTGTTGCTCTCTCTGAGAAAGATCTACTCTGAATT 1384  
DB 1197 GGTCTTGTCTCCGTTGAAGAAAGACCTGTACCTGAATT 1235  
RESULT 4  
ADU20461  
ID ADU20461 standard; cdNA; 1239 BP.



XX ADU20461;  
 AC 13-JAN-2005 (first entry)  
 DT  
 XX A. thaliana drought tolerance-associated cDNA At2g42690.  
 DE  
 XX ss; gene; plant; tolerance; resistance; environmental stress; drought.  
 XX Arabidopsis thaliana.  
 OS  
 FH Key Location/Qualifiers  
 FH CDS 1..1239  
 FT /\*tag= a  
 FT /product= "drought tolerance-associated protein"  
 PN W02004092349-A2.  
 XX  
 PD 28-OCT-2004.  
 PF 15-APR-2004; 2004WO-US011887.  
 XX  
 PR 15-APR-2003; 2003EP-00008079.  
 PR 01-AUG-2003; 2003EP-00016671.  
 PR 30-SEP-2003; 2003EP-00022226.  
 XX  
 PA (BADI ) BASF PLANT SCI GMBH.  
 PI Puzio P, Chardonmets A, Chen R, Puente P;  
 DR WPI: 2004-766856/75.  
 DR P-PSDB: ADU20462.  
 XX  
 PT New transformed plant cell with altered metabolic activity compared to a  
 PT corresponding non transformed wild type plant cell, useful for producing,  
 PT screening and breeding plants with increased tolerance to environmental  
 PT stress.  
 XX  
 PS Disclousure; SEQ ID NO 107; 607bp; English.  
 XX  
 CC This invention describes a method resulting in a novel transformed plant  
 CC cell which has been altered by an inactivated or down-regulated gene and  
 CC results in increased tolerance and/or resistance to an environmental  
 CC stress as compared to a corresponding non-transformed wild type plant  
 CC cell. The method can be used to generate or screen for seeds or plants  
 CC with increased tolerance/resistance to environmental stress and for  
 CC detecting stress in cells or plants. The transformed plant cell comprises  
 CC a metabolic activity that is altered concerning one or more metabolites  
 CC selected from 2,3-dimethyl-5-phytylquinol, 2-hydroxy-palmitic acid, 3,4  
 CC dihydroxyphenylalanine, 3-hydroxy-palmitic acid, 5-oxoproline,  
 CC alanine, alpha linolenic acid, alpha-tocopherol, amino adipic acid,  
 CC alanylglutamate, arginine, aspartic acid, beta-9p-81 carotenal, serine,  
 CC beta-carotene, beta-sitosterol, beta-tocopherol, hexadecatrienic acid,  
 CC margaric acid, gamma-aminobutyric acid, (delta-7-cis,10-cis)-  
 CC hexadecadienic acid, delta-15-cis-tetracosenic acid, ferulic acid,  
 CC campesterol, cerotic acid (c26:0), citrulline, cryptoxanthine, glucosonic  
 CC acid (20:1), fructose, fumarate, galactose, gamma-tocopherol, gluconic  
 CC acid, glucose, glutamic acid, glutamine, glycerate, glycerinaldehyde,  
 CC glycerol, glycerol-3-phosphate, glycine, homoserine, inositol,  
 CC isoleucine, iso-malose, isopentenyl pyrophosphate, leucine, lignoceric  
 CC acid (c24:0), linoleic acid (c18:2 (c9, c12)), luteine, lycopen, malate,  
 CC mannose, methionine, methylgalactofuranoside, methylgalactopyranoside,  
 CC methylgalactopyranoside, palmitic acid (c16:0), phenylalanine, phosphate,  
 CC proline, putrescine, pyruvate, raffinose, ribonic acid, threonine,  
 CC stearic acid (c18:0), succinate, sucrose, threonine,  
 CC triacontanoic acid, tryptophane, tyrosine, ubiquinone, udp-glucose,  
 CC valine, and zeaxanthine. The plant is selected from maize, wheat, rice,  
 CC oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola,  
 CC manihot, pepper, sunflower, flax, borage, safflower, linseed, primrose,  
 CC repressed, turnip rape, tagetes, solanaceous plants, potato, tobacco,  
 CC eggplant, tomato, Vicia species, pea, alfalfa, coffee, cacao, tea, Salix  
 CC species, oil palm, coconut, perennial grass, forage crops and Arabidopsis  
 CC thaliana. The environmental stress is selected from salinity, drought,

CC temperature, metal, chemical, pathogenic and oxidative stresses, or their  
 CC combinations. The inactivation or down-regulation of the gene is achieved  
 CC by double-stranded RNA interference (dsRNAi), introduction of an  
 CC antisense nucleic acid, a ribozyme, an antisense nucleic acid combined  
 CC with a ribozyme, a nucleic acid encoding a co-suppressor, a nucleic acid  
 CC encoding a dominant negative protein, DNA- or RNA- or protein-binding  
 CC factors targeting said gene or -RNA or -proteins, RNA degradation  
 CC inducing viral nucleic acids and expression systems, systems for inducing  
 CC a homolog recombination of the genes, mutations in the genes or their  
 CC combinations. This sequence represents a gene involved in drought  
 CC tolerance, isolated from Arabidopsis thaliana.  
 CC  
 XX  
 SQ Sequence 1239 BP; 346 A; 249 C; 323 G; 321 T; 0 U; 0 Other;  
 Query Match 22.9%; Score 351.4; DB 13; Length 1239;  
 Best Local Similarity 57.9%; Pred. No. 3.7e-73;  
 Matches 752; Conservative 0; Mismatches 466; Indels 81; Gaps 4;  
 QY  
 DB 89 CCCAATGAGCCCGAATCTCCGCGGTCCAATGCTTGGGCGGCTACTAAACCGCTCAA 148  
 15 CACATCATGGGAAGAACTCTTAGGCTCAAGAAATTGGGACACTTCTTAGCCATTAGA 74  
 QY 149 CGATGAGCTCCGTGAGCTCTCTTACGCTGCGGGAACTTCTGCCAGGTGACATACGAC 208  
 DB 75 CCAATCACTTAGGGAATCAATCTTACGTTGGGCGACTTTTGTCAAGCCACTACGATGC 134  
 QY 209 CTTGATTAAGACCAAGAACTGCTCTACTGCGGACGACCGCTTACCGGAAGGGGACCT 268  
 DB 135 CTTGTGTAAGACCAAGAACTGCTCTACTGCGGACGACCGCTTACCGGAAGGGGACCT 194  
 QY 269 ACTTCATAAGACCGCTTCCCGGGGGCGGACCGGCTTTGACGTGGGCGTACTTGTGA 328  
 DB 195 CTTGACAGAG--GTCTGTCTGCAAAACGCTTCGACCTACGAGTTTAACTTCTCTA 251  
 QY 329 CGCCACTGCGAAGGTGACGCTCCGAGAGCGTTCCTGCTGAGTGAAGTGAAGGAGAA 388  
 DB 252 CGCCAGAGCTGCTGTCTTCTCCCGAAGGTTTCTTCCATCAATCAATCAAGATTC 311  
 QY 389 GTGGGATGAGGAATCGAATTGATGATGGGTATGTGTGTGTCTGCAATGACGAGATCG 448  
 DB 312 TTGGGACCGGAGCTTCAATGCTTGTGCTACATTTGCTGACGCTGATGAACGGTCTAA 371  
 QY 449 GGTGGCGGAGCAAGGAGGATGTGTGTGTGAGAGGAGCTTGTAGGATTTAGATG 508  
 DB 372 GCTTTGAGAGCGCTGATGATCTATATAGCTTTGAGAGGAGCAAGCAATCTAGATG 431  
 QY 509 GGTGATGTTCTTGTGCTCACTTGAAGTGTGCTCATCTTTGTAAGCACTCAACAAAC 568  
 DB 432 GGTCAATGTTTGTGCTGTAGGCACTTGAAGTGTGCAAGTGTGCAAGGAGCA 491  
 QY 569 TACTCATGTTGAAAAGGTGAAAATGAGAAAAGAGAGCATTCATTAATCAAGTGGTA 628  
 DB 492 GGAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 520  
 QY 629 GCAATGTTTCAATTCAACTACCTAGGTTCCGCTCCAAAGCAAGAAAAGAGAGCA 688  
 DB 521 GCAATTTT-----GATAGGA 536  
 QY 689 GCAAGCAGATGATGACCAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 748  
 DB 537 CAGTGAAGATGAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 596  
 QY 749 GGAATCCAAATCACCTTCAAAAATTAAGTGAAGAACCAACTTCAAGCAAACTCAA 808  
 DB 597 TCACCCGGAATCGAATTCATTAAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 656  
 QY 809 ACAATTAATGACAAATTAACAAAGCAAAACCTTAAGATTAACATTCGCGCTCAACAGCT 868  
 DB 657 GGAATCTTCTGTGAAGTAAAGGACGAAACCGAGATTTGTGACTGACCTATACCTT 716  
 QY 869 AGGCGACACCTATCACTGCTGAGCGCTTCACTGATGAGAGAA--TCTCAAGACCGA 925  
 DB 717 GGAAGCTACAGAGCTGTTCTGCGCGCTTATGATGATGATGATGATGATGATGATGATG 776

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QY 926 GATCCAGTCACGGCCGCTGCTTCGCGGTGCCCAAAAGTAGCAACAACAAAATTCACACA 985
D 777 TGTTCCTCCGCTACTCTCTATAGTCTTGGTGTCCACAGTTAGAAACAAAGGTTCAAGGA 836
QY 986 ACTCTTCGACTCGTACCCAAACCTAAATGTCCTTCATGTAAAGAAATGTCATGACTGAT 1045
D 837 CGAAGTATAGTACCAAGAACTTAAAGATCCTCATGTAAAGAAACGATTTGATCTCTT 896
QY 1046 CCGCTCTGATCCCGTAAACCTCATAGGGTTAGTGAACATAGAAATCGAGCTGGATCGA 1105
D 897 AACTCGATACCCAGGGGACTTTTAGGGTATGTGACATAGAAATAACTTTGATCGA 956
QY 1106 CTCGAGGAAGTCGACCTTTCTAAAGAACTCGAAAAACCGAGTATGGCATTAATTTGCA 1165
D 957 TACAAAGAGTACACCGTTCTTAAGAGATTCAAGAAATCAGGGATTTGGCATTAATCTTCA 1016
QY 1166 AGCAATATTCGATGTTTGAAGTGTGGCATGGGGTTAAGGGGAGTTAAAGTTGTTAA 1225
D 1017 GGGCATGTATACATGTTGTAGCTGATGGATGGAAATGGGAAGAAAGATTAAACTGATGCT 1076
QY 1226 TAAAGAAAGTGTGCTGATTTGTTAATAGTCATGTGATTTTCTTAAGAAAGATGTTTGGT 1285
D 1077 TAAAGAAAGTATGCTATTAAGTGAACAGTCAATGCGAGTTCTTGAAAGCTGAGTGTGGT 1136
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D 1197 GGTTCCTGCTCTCTCTGTAAGAAAGAACTGTACTGTAATT 1235

RESULT 5
ADU20618
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AC ADU20618;
DT 13-JAN-2005 (first entry)
DE A. thaliana At2g42630 homologue DNA.
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KM gene; plant; tolerance; resistance; environmental stress; drought; ds;
OS Arabidopsis.
OS thaliana;.
FH
FT Key Location/Qualifiers
FT CDS 1..1239
FT /tag= a
FT /product= "putative lipase"

W02004092349-A2.
XX
PD 28-OCT-2004.
XX
PF 15-APR-2004; 2004WO-US011887.
XX
PR 15-APR-2003; 2003BP-00008079.
PR 01-AUG-2003; 2003BP-00016671.
PR 30-SEP-2003; 2003BP-00022226.
XX
PA (BADI ) BASF PLANT SCI GMBH.
PI Puzio P, Chardonens A, Chen R, Puente P;
DR WPI, 2004-766856/75.
DR P-PSDB; ADU20619.
XX
PT New transformed plant cell with altered metabolic activity compared to a

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PT corresponding non transformed wild type plant cell, useful for producing,
PT screening and breeding plants with increased tolerance to environmental
PT stress.
XX
PS Disclosure; Page 579; 607pp; English.
XX
XX This invention describes a method resulting in a novel transformed plant
CC cell which has been altered by an inactivated or down-regulated gene and
CC results in increased tolerance and/or resistance to an environmental
CC stress as compared to a corresponding non-transformed wild type plant
CC cell. The method can be used to generate or screen for seeds or plants
CC with increased tolerance/resistance to environmental stress and for
CC detecting stress in cells or plants. The transformed plant cell comprises
CC a metabolic activity that is altered concerning one or more metabolites
CC selected from 2,3-dimethyl-5-phytylquinol, 2-hydroxy-palmitic acid, 3,4
CC dihydroxyphenylalanine, 3-hydroxy-palmitic acid, 5-oxoprolin,
CC alamine, alpha linolenic acid, alpha-tocopherol, aminoaliphatic acid,
CC anhydrotolucose, arginine, aspartic acid, beta-apo-81 carotenal, berine,
CC beta-carotene, beta-sitosterol, beta-tocopherol, hexadecatrienic acid,
CC margaric acid, gamma-aminobutyric acid, (delta-7-cis,10-cis)-
CC hexadecadienic acid, delta-15-cis-tetradecenoic acid, ferulic acid,
CC campesterol, cerotic acid (c26:0), citrulline, cryptoxanthine, eicosenoic
CC acid (20:1), fructose, fumarate, galactose, gamma-tocopherol, gluconic
CC acid, glucose, glutamic acid, glutamine, glycerate, glycerinaldehyde,
CC glycerol, glycerol-3-phosphate, glycine, homoserine, inositol,
CC isoleucine, iso-maltose, isopentenyl pyrophosphate, leucine, lignoceric
CC acid (c24:0), linoleic acid (c18:2 (c9, c12)), luteine, lycopen, malate,
CC mannose, methionine, methylgalactofuranoside, methylgalactopyranoside,
CC methylgalactopyranoside, palmitic acid (c16:0), phenylalanine, phosphate,
CC proline, putrescine, pyruvate, raffinose, ribonic acid, shikimate,
CC sinapline acid, stearic acid (c18:0), succinate, sucrose, threonine,
CC triacontanoic acid, tyriophane, tyrosine, ubiquinone, udp-glucose,
CC valine, and zeaxanthine. The plant is selected from maize, wheat, rice,
CC oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola,
CC manihot, pepper, sunflower, flax, borage, safflower, linseed, primrose,
CC rapeseed, turnip rape, tagetes, solanaceous plants, potato, tobacco,
CC eggplant, tomato, Viola species, pea, alfalfa, coffee, cacao, tea, Salix
CC species, oil palm, coconut, perennial grass, forage crops and Arabidopsis
CC thaliana. The environmental stress is selected from salinity, drought,
CC temperature, metal, chemical, pathogenic and oxidative stresses, or their
CC combinations. The inactivation or down-regulation of the gene is achieved
CC by double-stranded RNA interference (dsRNAi), introduction of an
CC antisense nucleic acid, a ribozyme, an antisense nucleic acid combined
CC with a ribozyme, a nucleic acid encoding a co-suppressor, a nucleic acid
CC encoding a dominant negative protein, DNA- or RNA- or protein-binding
CC factors targeting said gene or -RNA or -proteins, RNA degradation
CC inducing viral nucleic acids and expression systems, systems for inducing
CC a homolog recombination of the genes, mutations in the genes or their
CC combinations. This sequence represents a homologue of an Arabidopsis
CC thaliana drought tolerance gene.
XX
SQ Sequence 1239 BP; 346 A; 249 C; 323 G; 321 T; 0 U; 0 Other;

Query Match 22.9%; Score 351.4; DB 13; Length 1239;
Best Local Similarity 57.9%; Pred. No. 3.7e-73;
Matches 752; Conservative 0; Mismatches 466; Indels 81; Gaps 4;

QY 89 CCCAAGATGGGCCGACCTCCGCGGTCCAAATGCTTGGCGCGGACTTACCTAAACCCGCTCA 148
D 15 CACATCATGGAGAGAACTCTTAGGCTCAAAAGAAATTTGGACACTATCTTAGACCACTTAA 74
QY 149 CGATGAGCTCCGTGAGCTCTCTACGCTGGCGGAGACTTTCGCCAGTGAATACGACAC 208
D 75 CCAATCACTTGGAGAACTCATCTTAAGTGTGGGACATTTGTCAAGCACACTAGAGATG 134
QY 209 CTTCAATAAGCAACGAAGTGTCTTACTGTGGGACGACGCGCTACCGGAAAGCGGAGACT 268
D 135 CTTGCTCAAGCAACCAAACTCCAAAGTACTGTGGAGCCGCGCTACCGGAAATCTTCTTT 194
QY 269 ACTTCATAAGACCGGCTCCGCGGGGCGGAGACCGGTTTGACGTTGAGGCTACTTGTGA 328
D 195 CTTGCAAG--GTCATGCTGAAAAACGCTTCGACTACAGAGTTGTAACTTCTCTTA 251

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QY 389 GTGGGATGAGGATCGAATTGGATTGGTATGCTGTGTGTCGAATGACGACGAGTCG 448  
DB 312 TTGGGACCGTGAAGCTAAGTGGTTCATGTGCTGCTGCTGATGAGAACCGTCTAA 371  
QY 449 GGTGGCGGAGCGAAGGGAGGTGATGCTGTGAGAGGAGCTTGTGGGATTAATGAGTG 508  
DB 372 GGGCTTGAAGAGCCGTGAGATCTATATAGCTTTAGAGAGAAAGAGCGAGAACTATGAGTG 431  
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DB 432 GGTCAATGTTTGGGTCTAGGCGCACTGAGTGAACCCCTGTGTCAGCGAACCGGACA 491  
QY 569 TACTCATGTTGAAAAGGTGAAAAATGAGAAAAGAACATTCATTAATCAAGTTGGTA 628  
DB 492 GGAATGTTCTGTGTGTGTTGAA-----GGTAA 520  
QY 629 CGACTGTTCAATTCACACCTAGGTTCCGCGTCCAAAGACAAAGAAAAGGAGCGA 688  
DB 521 CGACTTTT-----GATAGTGA 536  
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DB 537 CAGTGAAGATGAGAAAGGTGTATAGTGTCTGGGGGTGCTCAATCTATATTTCTAA 596  
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DT 17-OCT-2000 (first entry)  
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35449.  
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KM Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway; metabolic pathway;  
KM promoter; termination sequence; ss.  
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OS Arabidopsis thaliana.  
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EN EP1033405-A2.  
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PD 06-SEP-2000.  
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PF 25-FEB-2000; 2000EP-00301439.  
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Query Match 22.9%; Score 351.4; DB 3; Length 1259;  
Best Local Similarity 57.9%; Pred. No. 3.7e-73;  
Matches 752; Conservative 0; Mismatches 466; Indels 81; Gaps 4;

QY 89 CCACATGCGCCGAACTCTCGGGTCCATGCTTGCGCCGGGCTACTAAACCCGCTCA 148  
DB 35 CACATCATGGAGAACTCTTAGGCTCAAGAAATTGGGACACTACTTAAACCCATTGA 94  
QY 149 CGATGAGCTCCGTGAGCTCTCTCTACGCTGCGGGGACTTCTGCCAGGTGACATACGAC 208  
DB 95 CCAATCACTTAGGGAATCATCTTACGTTGGGCGACTTTGTGTAAGCCACACTACGATGC 154  
QY 209 CTTCAATAACGACCAACTGCTCTACTTGCGGACGACCCGCTACCGGAAAGCGGACCT 268  
DB 155 CTTGCTCAACGACCAAACTCAAGTACTGTGGAGCCGCGCTACGGCAATCTTTCTT 214

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Qy 269 ACTTCATTAAGACCCGCTTCCCGGGGGGCGACACCGGTTTGACGTGTGCGCTACTTGTGA 328
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Qy 389 GTGGAGTAAGGAAATCGAATTTGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 448
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Qy 449 GGTGGCGGAGCGAAGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 508
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Qy 629 CGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 688
Db 541 CGACTTTT-----GATATGTGA 556
Qy 689 CGACGACGATGATGACGACCCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 748
Db 557 CAGTGAAGATGAAAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 616
Qy 749 GGATCCCAATCACCTTTCACAAAATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 808
Db 617 TCACCCCGAATCGAATTCCTAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 676
Qy 809 ACACTATATGACAAATATCAAGACGAAACCTTAAGCATTAATTCGCGGTGTGTGTGTGTGT 868
Db 677 GGAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 736
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Qy 1166 AGCAATATGTGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1225
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Db 1217 GGTTCCTTGTCCGCTTGAAGAGAAACCTGTATCTGAATTT 1255
RESULT 7
ID AAA53885 standard; DNA; 1167 BP.
XX
AC AAA53885;
XX
DT 03-JAN-2001 (first entry)
XX
DE Arabidopsis EST showing 55/5% homology with senescence induced.
XX
KM Senescence-induced lipase; senescence; lipase; antisense; regulation;
XX modulation; resistance; stress; crop protection; ethylene; ds.
XX Arabidopsis thaliana.
FH Key Location/Qualifiers
FT CDS 1..1047
FT /*tag= a
FT /label= EST
XX
PN MO200049164-A1.
XX
PD 24-AUG-2000.
XX
PF 14-FEB-2000; 2000MO-US003494.
XX
PR 16-FEB-1999; 99US-00250280.
XX
PA (SENESC-) SENESCO INC.
XX
PI Thompson JE, Wang T, Hudak K, Hong Y,
XX
DR WPI: 2000-549277/50.
XX P-PSDB: MAY97308.
XX
PT DNA encoding carnation senescence-induced lipase, useful for regulating
PT the expression of senescence in plants to delay its onset and improve
PT plant resistance to environmental stress, thus extending shelf-life or
PT growth period.
XX
PS Disclosure; Fig 13; 89pp; English.
XX
CC Insertion of the senescence-induced lipase coding sequence in an
CC antisense direction in a plant genome can be used to regulate the
CC expression of senescence in those plants. Alteration of expression of the
CC senescence-induced lipase gene in plants results in delayed onset of
CC senescence and improved resistance to environmental stress, thus
CC extending the plant shelf-life and/or growth period. The genetically
CC altered plant is useful for producing a new variety or line of plants
CC where the alteration is stably transmitted from generation to generation.
CC This method of regulation is advantageous over prior senescence
CC modulating technologies since prior methods were only applicable to a
CC limited range of plants, e.g. to plants that are ethylene-sensitive. The
CC antisense regulation method is applicable to all types of plants,
CC regardless of ethylene sensitivity
XX
SQ Sequence 1167 BP; 338 A; 213 C; 305 G; 311 T; 0 U; 0 Other;
Query Match 18.9%; Score 291.2; DB 3; Length 1167;
Best Local Similarity 64.3%; Pred. No. 7.4e-59;
Matches 453; Conservative 0; Mismatches 248; Indels 3; Gaps 1;
Qy 684 AGGAGACGACGACGATGACGACCCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 743
Db 340 AGTACAGTGAAGTGAAGAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 399
Qy 744 TCGGAGATCCCAATCAACCTTTCACAAAATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 803
Db 400 TCTATATACCCCGAATGGAATTCATTAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 459

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QY 1281 TTGGTTCCTCCAGCTTGGTGGTGTGTGCAGAACAAAGGATGTTTTGAATPAAGATGCT 1340  
 DB 940 TTGGTTCAGAGATCTTGGTGGTGTAGAGAAACAAGACTGATCAAGAAAGAGATGCT 999  
 QY 1341 GAGTGGGTTTGGTCTCTCTGAGGAAGATCTTACTCTGAATT 1384  
 DB 1000 GAATGGGTTCTTGGCTCCCGTTGAAGAAACCTGTACTGAATT 1043

RESULT 9  
 ACL26423  
 ID ACL26423 standard; cDNA; 1077 BP.  
 XX ACL26423;  
 AC  
 XX  
 DT 02-JUN-2005 (first entry)  
 XX  
 DE Rice abiotic stress responsive polynucleotide SEQ ID NO:379.  
 XX  
 KM ss; abiotic stress tolerance; transgenic plant; plant; cereal;  
 XX agriculture.  
 OS Oryza sativa.  
 XX  
 PN MO2003008540-A2.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002WO-US019668.  
 XX  
 PR 22-JUN-2001; 2001US-0300112P.  
 PR 24-AUG-2001; 2001US-0314662P.  
 PR 26-SEP-2001; 2001US-0325277P.  
 PR 21-NOV-2001; 2001US-0332132P.  
 XX  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;  
 PI Moughamer T, Provart N, Ricke D, Zhu T;  
 XX  
 DR WPI; 2003-248011/24.  
 XX  
 PT New stress-responsive nucleic acid, useful for altering the  
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold  
 PT stresses, salt stress or osmotic stress.  
 XX  
 PS Claim 1; SEQ ID NO 379; 89pp; English.  
 XX  
 CC The invention relates to novel abiotic stress responsive polynucleotides  
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host  
 CC cells, and plants containing such polynucleotides. Also disclosed are  
 CC methods for using the polynucleotides and polypeptides to alter the  
 CC responsiveness of a plant to abiotic stress. The invention is useful in  
 CC agriculture. The nucleic acid is useful for determining whether a test  
 CC plant has been exposed to an abiotic stress condition. It is also useful  
 CC for selecting an agent that alters abiotic stress regulated  
 CC polynucleotide expression in a plant cell, and to identify a homolog or  
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid  
 CC molecule and the polypeptide encoded by it are useful in altering the  
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt  
 CC stress, osmotic stress or any of their combinations. The present sequence  
 CC is used in the exemplification of the invention

QY 693 GACGATGATGACGACCCCAAGTATGCAAGGTGATGACAAATATACATCGAGAT 752  
 DB 397 GGCAGTCTGATGACCCCTTGTGTGATGGGGGGGCTGTCTGTGTACACGAGTCCGAT 456

Query Match 11.0%; Score 169.4; DB 11; Length 1077;  
 Best Local Similarity 55.2%; Pred. No. 6.6e-30;  
 Matches 376; Conservative 0; Mismatches 296; Indels 9; Gaps 2;

QY 753 CCCAATCACCCTTTCACAAAATAAGTGAGAACACAACTCTAGACCAACTCAACAA 812  
 DB 457 CCAAAATCTCAGTACAAATTAAGAGAGTGCAAGATATCAGGCTTGAATGAGATCAAAACGG 516  
 QY 813 CTAATGCAAAATATCAAAAGAGCAAAACCTTAAGCATTAATTCGCGGTCAAGCTTAGGC 872  
 DB 517 CTCGAGATATGTACGAGCATGAGAGACTAGCATTCACATTAACAGGCGACAGCTTGGG 576  
 QY 873 GCGACACTATCAGTGTGAGGCGCTTGACATAGTGGAGATCTCAAGACCGAGATC--- 929  
 DB 577 GCTGCACTTGGCACCATCAATATCCACTGACATTTGTCTTCAATGGTTACACAAAGCTGT 636  
 QY 930 CCAATCAGCGCGGTGTCTTTCGGGTGCCCAAAAGTAGGCAACAAAAATTCACAACTC 989  
 DB 637 CCAATGTCTGCTTGTGCTTGTGTAGCCCAAGAGTGGGCAACCTGATTTTCAGAAACGG 696  
 QY 990 TTGACCTGTACCCAACTTAATGTCTCTCATGTAAAGAAATGTCATGACCTGATCCTT 1049  
 DB 697 TTGCACAGTGTCTCCAGATTTGAGATTGCTCCGCAATCGAAACTCTCCTGATGTGATCCA 756  
 QY 1050 CTGTATCCCGTGAACATCATGGGTTAGTGAACATAGGAATCGAGCTGAGATGACTCG 1109  
 DB 757 AACTGSC-----AAACTAGATACAGCGATCTGACAGAGCTGATGATGATGACA 810  
 QY 1110 AGGAATGCACTTTCTTAAAGACTCGAAAAACCCGAGTATGTCATTAATTTGCAAGCA 1169  
 DB 811 GCGAAGTACCATATCTGGAAGGCCCTTGGGAATCCCTAAGTGGCATGATGAGATGCG 870  
 QY 1170 ATATTCATGTGTGAATGTGTGTCATGGGCTTAAGGGGAGTTTAAAGTTTGAATPAAG 1229  
 DB 871 TACATGATGAGGGGTGGCGGGGACGCAAGGAGCAACGAGGGTTCAAGCTGAGATGATGAT 930  
 QY 1230 AGAAGTTCATGTGTGAATTAATCAATGATTTTCTTAAAGAAAGATGTTGGTTCCT 1289  
 DB 931 CGAACAATGTCTTGTGTTAACAAACAGAAACGCACTGAAGATGATGCAATTCACA 990  
 QY 1290 CCAAGTTGTGGGTGTGTCAGAACAAAGGATGTTTGAATAGATGATGAGTGGTT 1349  
 DB 991 TCGTCTGTGTGGTGTGTCAGAACAAAGATGATGATGATGATGATGATGATGATGAT 1050  
 QY 1350 TTGGCTCTCTCTGAGGAAGAT 1370  
 DB 1051 TTGGCCGACATGAGATGAT 1071

RESULT 10  
 ACL26207  
 ID ACL26207 standard; cDNA; 1533 BP.  
 XX  
 AC ACL26207;  
 AC  
 XX  
 DT 02-JUN-2005 (first entry)  
 XX  
 DE Rice abiotic stress responsive polynucleotide SEQ ID NO:163.  
 XX  
 KM ss; abiotic stress tolerance; transgenic plant; plant; cereal;  
 XX agriculture.  
 OS Oryza sativa.  
 XX  
 PN MO2003008540-A2.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002WO-US019668.  
 XX  
 PR 22-JUN-2001; 2001US-0300112P.  
 PR 24-AUG-2001; 2001US-0314662P.  
 PR 26-SEP-2001; 2001US-0325277P.  
 PR 21-NOV-2001; 2001US-0332132P.  
 XX  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

PI Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,  
 XX Moughamer T, Provart N, Ricke D, Zhu T;  
 DR WPI; 2003-248011/24.  
 XX  
 PT New stress-responsive nucleic acid, useful for altering the  
 XX responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold  
 XX stresses, salt stress or osmotic stress.  
 PS Claim 1; SEQ ID NO 163; 899p; English.  
 XX  
 CC The invention relates to novel abiotic stresses responsive polynucleotides  
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host  
 CC cells, and plants containing such polynucleotides. Also disclosed are  
 CC methods for using the polynucleotides and polypeptides to alter the  
 CC responsiveness of a plant to abiotic stress. The invention is useful in  
 CC agriculture. The nucleic acid is useful for determining whether a test  
 CC plant has been exposed to an abiotic stress condition. It is also useful  
 CC for selecting an agent that alters abiotic stress regulated  
 CC polynucleotide expression in a plant cell, and to identify a homolog or  
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid  
 CC molecule and the polypeptide encoded by it are useful in altering the  
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt  
 CC stress, osmotic stress or any of their combinations. The present sequence  
 CC is used in the exemplification of the invention  
 XX  
 SQ Sequence 1533 BP; 278 A; 546 C; 463 G; 246 T; 0 U; 0 Other;

Query Match 10.8%; Score 165.6; DB 11; Length 1333;  
 Best Local Similarity 54.5%; Pred. No. 6.1e-29;  
 Matches 367; Conservative 0; Mismatches 289; Indels 18; Gaps 1;

QY 714 GTGATGCAAGGTGGATGACATATACATCGAGGAGTCCCAATTCACCTTCACAA 773  
 DB 709 GTCATGAAGGGGTGTACTTACTTACAGCTCCAGCCGAGCGCTCCCTTTCTCCAG 768  
 QY 774 CTAAGTGCAGAAACCACTTCAAGCAACTCAAACTAATATGACAAATACAAAGAC 833  
 DB 769 TACAGCGCCCGACCAATGTGCGCCCGTGGCGAGCTGTGGCGAGTACGAGAAC 828  
 QY 834 GAAACCTTAAGCATTAATTCGCGGTGACAGCTTAAGCGCGGACATATCACTGTGAGC 893  
 DB 829 GAGAGCCTCGGCTGTGTGCAACGGGGACAGCCTCGGCGCTCCCTGCCACGCTCTGC 888  
 QY 894 GCCTTCGACATATGTGGAATATCTCAGACCGAG-----ATCCCATGC 935  
 DB 889 GCGTTCATATGTGTGTCAACGGCGGTGTCAAGTGGCGACGCGCGCACATTCGGGTG 948  
 QY 936 ACGCGCGTGTCTTGGGTGCCCAAAAGTAGGCAACAAAATTTCCAACTTCTTCGAC 995  
 DB 949 ACCGCGGTGTGTTCGGAGCCCGAGATCGGGAATCCGGAGTTCAAGAGAGATTCCAG 1008  
 QY 996 TCGTACCAAACTTAATATGTCTCATATGAGAAATGTCATGACCTGATCCCTGTGAT 1055  
 DB 1009 GAGCAGCCCAACTCTCGGGCGCTGCACGTCAAGAAATGCCCCGACTCCCGCTTAC 1068  
 QY 1056 CCCGGAATTCATGAGGTGTAACCTGAACATAGGAATCGAGCTGAGATGACTCGAGAG 1115  
 DB 1069 CCGAGCGGCTCTCTGGCTACCGCAACGTGGCAAAACCTTCAGAGTCACTTCAAGAG 1128  
 QY 1116 TCGACCTTCTTAAGAGACTCGAAAAACCGAGTGAATTGGCATTAATTTGCAAGCAATAT 1175  
 DB 1129 TCGCCCTTACGTAAACGAGACACCGAGCCGAGCTACCAACCTCGAGGGAGTCTTA 1188  
 QY 1176 CATGTTGAATGTGTGGCATGGGGTTAAGGGGAGTTTAAGGTTGAATTAAGAAAGT 1235  
 DB 1189 CACACGGTGGCGGCTGGAAACGGGAAGACGCGCATTCAGCTCAGGTGAAGCGCAGC 1248  
 QY 1236 GTTGATGTTGTTAATTAAGTCAATGATTTCTTAAGAAAGATGTTGGTCTCTCAGCT 1295  
 DB 1249 GTTCGGCTGTGTAAACAAAGTGAAGCGGCTTCTTCAAGGACAGCACTTGTGCGAGTGA 1308  
 QY 1296 TGGTGGTGTGTGCAAAACAAAGGAGTGTGTTGAATTAAGATGTGAGTGGGTTTGGCT 1355

DB 1309 TGGTGGTGTGTGAGGAAACAAAGCATGTGCTGGCCAGAACGGGGATGCGACTCGAG 1368  
 QY 1356 CTCCTGAGGAGA 1369  
 DB 1369 GGGCCCGCAGAGCA 1382

RESULT 11  
 ADA71310  
 ID ADA71310 standard; DNA; 2064 BP.

AC ADA71310;  
 XX 20-NOV-2003 (first entry)  
 DT  
 XX Rice gene, SEQ ID 4633.

DE Plant; bacterial infection; fungal infection; viral infection; rice;  
 KW gene; ds.

OS Oryza sativa.

XX WO2003000898-A1.

PD 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
 XX WPI; 2003-175290/17.

PT Identifying at least one gene involved in plant resistance or response to  
 PT pathogenic infection for conferring resistance or tolerance to a plant to  
 PT bacterial, fungal or viral infection by determining or detecting plant  
 PT gene expression.

PS Claim 6; SEQ ID NO 4633; 899p; English.

XX The present invention relates to a method (M1) for identifying genes  
 CC involved in plant resistance or response to pathogenic infection. M1  
 CC comprises identifying a gene whose expression is significantly altered in  
 CC the incompatible interaction of plant gene expression relative to  
 CC expression of the gene in an uninfected plant, in a mutant plant that  
 CC does not express a gene associated with response to pathogenic infection,  
 CC or in a corresponding incompatible or compatible interaction. (M1) is  
 CC useful for conferring resistance to resistance or tolerance to a plant to  
 CC bacterial, fungal or viral infection. The present sequence was used to  
 CC illustrate the invention.

SEQ Sequence 2064 BP; 423 A; 644 C; 624 G; 373 T; 0 U; 0 Other;

Query Match 10.8%; Score 165.6; DB 8; Length 2064;  
 Best Local Similarity 54.5%; Pred. No. 6.8e-29;  
 Matches 367; Conservative 0; Mismatches 289; Indels 18; Gaps 1;

QY 714 GTGATGCAAGGTGGATGACATATATACATCGAGGATCCCAATTCACCTTCACAA 773  
 DB 1240 GTCATGAAGGGGTGTACTTACTTACAGCTCCAGCCGAGCGCTCCCTTTCTCCAG 1299  
 QY 774 CTAAGTGCAGAAACCACTTCAAGCAACTCAAACTAATATGACAAATTAAGAAAGAC 833  
 DB 774 TACAGCGCCCGACCAATGTGCGCCCGTGGCGAGCTGTGGCGAGGTACAGAGAAC 1359  
 QY 834 GAAACCTTAAGCATTAATTCGCGGTGACAGCTTAAGCGCGGAGCACTATCACTGTGAGC 893  
 DB 1360 GAGAGCCTCGGCTGTGTGCAACGGGGACAGCCTCGGCGGTGTGCTGCCACGCTCTGC 1419



QY 894 GCCTTCACATAGTGAGAAATCTCACGACCGAG-----ATCCCAATC 935  
 DB 1420 GCGTTCATATCGTCGTCAACGGGCTGCCAAGTCCGCCACGGCGCCGACATCCCGGTG 1479  
 QY 936 ACCGCGCGTGTCTTTCGGGTGCCCAAAAGTAGCAACAAAAATTCCAACTCTTCGAC 995  
 DB 1480 ACCCGCGTGTGTTCGGGAGCGCCGACATCGGAAACCGGAGTTCAAGAACAGTTCCAG 1539  
 QY 996 TCGTACCAACCAACCAATATCTTCATGTATAGTAATGCATGCACTGCATCCCTCTGAT 1055  
 DB 1540 GAGCAACCCCAACCTGCGGCGCTGCAGTCAAGAACATGCCGACCTCATCCGCTCTAC 1599  
 QY 1056 CCCGTGAACCTCATGGGTTCATGTAACATAGAAATCGAGTGCAGATCGACTCGAGAA 1115  
 DB 1600 CCGAGCGGCGCTCTTCGGCTAGCCCAACGTCCGCAAAACCTCCAGGTGACTCCAAAGAG 1659  
 QY 1116 TCGACCTTTCTTAAAGACTCGAAAAACCCGAGTATGGCATTATTTGCAAGCAATATG 1175  
 DB 1660 TCGCCCTACGTGAAGCGAGACACACAGCCCAAGCGACTACCAACCTGCAAGGGATCCTA 1719  
 QY 1176 CATGTTGTAAGTGTGGTTCATGGGTTTAAAGGGGAGTTTAAAGTTTAAATTAAGAAAGT 1235  
 DB 1720 CACACGCTGCGCGCTGGAACGGGAAGACCGCCAGTTCAAGCTCCAGTGAACCGCAGC 1779  
 QY 1236 GTTGCAATTGTTAATAGTCAATGATTTTCTTAAAGGAAGAAATGTTGTTCTCCAGCT 1295  
 DB 1780 GTCCGCTGTGTAACAAATGTCAGCGGCTTCTCAAGGACAGCAACCTTGTCGGAGTCA 1839  
 QY 1296 TGTGTGTTGTGCAAAACAAAGGATGTTTGAATAGATGTTGAGTGGTGGTTTGGCT 1355  
 DB 1840 TGTGTGTTGTGAGAGAAACAAAGCATGTGTCTCGGCCCAAGACGGGAATGCACTCGAG 1899  
 QY 1356 CTTCTTGAAGAA 1369  
 DB 1900 GGGCCCGCAGAGGA 1913

## RESULT 12

ADK60584  
 ID ADK60584 standard; cDNA; 1384 BP.

AC ADK60584;

DT 21-APR-2005 (first entry)

XX Plant full length insert polynucleotide seqid 31427.

XX plant protectant; plant growth regulant; gene therapy; plant;

KM recombinant DNA construct; physical array; plant breeding marker;

KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

KM extreme osmotic condition; pathogen tolerance; pest tolerance;

KM growth rate; cell cycle pathway; disease resistance;

KM galactomannan production; lignin production; plant growth regulator;

KM yield; plant growth; plant development; seed oil; protein yield;

KM protein content; gene; ss.

XX Unidentified.

OS US2004034888-A1.

PN 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

PR 05-NOV-2001; 2001US-00985678.

XX (LIU/J) LIU J.

PA (ZHOU/J) ZHOU Y.

PA (KOVA/J) KOVALIC D K.

PA (SCRE/J) SCREEN S E.

PA (TABAK/J) TABASKA J E.

PA (CAO/J) CAO Y.  
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 XX WPI: 2004-180133/17.  
 DR New recombinant DNA construct, useful for improving plant tolerance to  
 XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 XX Claim 1, SEQ ID NO 31427, 15pp; English.  
 PS  
 XX The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC <http://seqdata.uspto.gov/sequence.html?docid:2004034888>. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This sequence represents a plant full length insert  
 CC polynucleotide that can be used in the recombinant DNA construct of the  
 CC invention.  
 XX  
 SQ Sequence 1384 BP; 352 A; 330 C; 408 G; 294 T; 0 U; 0 Other;

Query Match 9.8%; Score 151; DB 13; Length 1384;  
 Best Local Similarity 53.8%; Pred. No. 1,7e-25;  
 Matches 363; Conservative 0; Mismatches 300; Indels 12; Gaps 2;

QY 702 GAGCAACCCCAAGATGCAAGTTGGATGCAATATACATCGGAGATCCCAATCA 761  
 DB 556 GCCAACCCCTGTGTGATGAGGAGGTGGCTTTCAGTCTACACGAGTGTGATCCAGGGTCA 615  
 QY 762 CCCTTGACAAATCTAAGTGCAGAAACAACTTCAGACCAAACTCAAACTAATGACA 821  
 DB 616 CAGTACAAACAAAGAGACCGCAAGCATCAAGTGTAAACGAGGTGAAGAAAGATACAGAT 675  
 QY 822 AATACAAAGACGAACCTTAAGCATTAATTCGCCCGGTCAACAGCTTAGGGCGACACTA 881  
 DB 676 CTGTACAAAGCAAGAGAGAGAGATCATCAATACAGGCCACTTAGAGAGACACTT 735  
 QY 882 TCACTGTGAGCGCTTCGACATAGT-----GAGAAATCTACAGACCGAGATCCCAATG 935  
 DB 736 GCGACCATCAACGCAACCGCATGTCTCCAAACGGCTACCAACAGAGACTGTGCTCGTGTG 795  
 QY 936 ACGGCGGTGTCTTCGGGTGCCCAAAAGTAGGCAACAAAATTCACAACTCTTGAC 995  
 DB 796 TCGCGTTCTGTATTCGAGAGCCCAAGTGGAAACCTTGATTTTCCAGAAAGCGTTGAC 855  
 QY 996 TCGTACCAACCTAATATGCTTCATGTAAAGATGATCATGCACTGATCCCTGTAT 1055  
 DB 856 AGCGCGGCGGACCTGAGAGCTGTCTCGGTCCGAACTCTCCGACGATGATCCCAATG 915  
 QY 1056 CCGGTGAACCTCATGGTTACGTGACATAGAAATGCACTGAGATGACATCGAGAG 1115  
 DB 916 CCAAG-----CTAGGTACAGTATGTGCGCAACAGCTGATGATGACACAGAGAA 969  
 QY 1116 TCGACCTTTCTTAAAGACTGGAATAACCCGAGTATGGCATATTTTCAAGCAATATG 1175  
 DB 970 TCGCGTACCTGAAGGCGCTTCGAAACCCCTGCATGACATGACATGACATGCTAATG 1029  
 QY 1176 CATGTTGTAAGTGTGGCATGAGGGTTAAGGGGAGTTTAAAGTTTAAATTAAGAAAGT 1235  
 DB 1030 CACGGGTCCTGTGGGCTCAAGGGGAGAGGGAGTTGACGTGTTGTCGATCGGAGAC 1089

QY 1236 GTTCATTGTTAATAGTCATGATTTTCTTAAGAAAGATGTTGTTCTCCAGCT 1295  
 DB 1090 GTTCTTTGTTGAAACAGCATGAAAGATCCCTGAGAAATGATTCGCTGCTCCACCGCG 1149  
 QY 1296 TGTGTGGTGTGCAACAAAGGATGTTTGAATAAGATGTTGAGTGGGTTTGCT 1355  
 DB 1150 TGTGTGGTGTGCAACAAAGGATGTTTGAATAAGGCAAGATGGCCGGTGGCATCTGGCC 1209  
 QY 1356 CCTCCTGAGCAAGAT 1370  
 DB 1210 GACCATGAGGAGAT 1224

RESULT 13  
 ID AAS3884 standard; DNA; 923 BP.  
 AC AAS3884;  
 XX  
 DT 03-JAN-2001 (first entry)  
 XX  
 DE Senescence-induced lipase partial coding sequence.  
 KM Senescence-induced lipase; senescence; lipase; antisense; regulation;  
 KW modulation; resistance; stress; crop protection; ethylene; ds.  
 OS Lycopersicon esculentum.

XX Key Location/Qualifiers  
 FH exon 6..512  
 FT /\*tag= a  
 FT /label= Exon 1  
 FT 513..842  
 FT /\*tag= b  
 FT /label= Intron 1  
 FT 843..921  
 FT /\*tag= c  
 FT /label= Exon 2

XX WO20049164-A1.  
 XX  
 PD 24-AUG-2000.  
 XX  
 PF 14-FEB-2000; 2000MO-US003494.  
 XX  
 PR 16-FEB-1999; 99US-00250280.  
 XX  
 PA (SENE-) SENESCO INC.  
 XX  
 PI Thompson JE, Wang T, Hudak K, Hong Y;  
 XX  
 XI WPI; 2000-549277/50.  
 DR P-PSDB; AAY97303.  
 XX  
 XX  
 PT DNA encoding carnation senescence-induced lipase, useful for regulating  
 FT the expression of senescence in plants to delay its onset and improve  
 PT plant resistance to environmental stress, thus extending shelf-life or  
 PT growth period.  
 XX  
 PS Disclosure; Fig 10; 89p; English.

CC Insertion of the senescence-induced lipase coding sequence in an  
 CC antisense direction in a plant genome can be used to regulate the  
 CC expression of senescence in those plants. Alteration of expression of the  
 CC senescence-induced lipase gene in plants results in delayed onset of  
 CC senescence and improved resistance to environmental stress, thus  
 CC extending the plant shelf-life and/or growth period. The genetically  
 CC altered plant is useful for producing a new variety or line of plants  
 CC where the alteration is stably transmitted from generation to generation.  
 CC This method of regulation is advantageous over prior senescence  
 CC modulating technologies since prior methods were only applicable to a  
 CC limited range of plants, e.g. to plants that are ethylene-sensitive. The

CC antisense regulation method is applicable to all types of plants,  
 CC regardless of ethylene sensitivity  
 XX  
 SQ Sequence 923 BP; 315 A; 148 C; 181 G; 279 T; 0 U; 0 Other;  
 Query Match 8.6%; Score 131.8; DB 3; Length 923;  
 Best Local Similarity 58.2%; Pred. No. 5.5e-21;  
 Matches 251; Conservative 0; Mismatches 177; Indels 3; Gaps 1;

QY 666 AAAGCAAAAGAAAGAGAGACGACGATGATGACGACCCCAAGTATGATCAAGT 725  
 DB 90 AACACAAAGAACGATGAGATGAGACGAGACGAGATGATCAAGTATGATGAGTGG 149  
 QY 726 TGGATGCAATATACATGCGAGAGATCCCAATGACCTTACAAATCTAATGTCAGA 785  
 DB 150 TGGCTTAAGATCTACGCTCAAGTAAACCGAAGTCGCTTTCACGAGACTAATGTCAGA 209  
 QY 786 ACACAACTTACAGCAACCAATCAACCTAATGCAAAATTCAAAGACGAAACCTTAAGC 845  
 DB 210 GAACAACTTCAAGCAAGATTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGC 269  
 QY 846 ATACATTGCGCGGTCAAGGCTGAGCGGCACTATCACTGATGAGCGCCTTGCACATA 905  
 DB 270 ATAACTTTACAGGCAATGCTTGTGCTAGCTTATGCTTATGATGATG 329  
 QY 906 GTGAGAA---TCTACAGACGAGATCCAGTCAAGCCGCTGCTTGGGTCGCAAAA 962  
 DB 330 GTTGAATGCTGTCAGAGTGAATTCAGATATCTGCAATGTATTTGTAATGCCAA 389  
 QY 963 GTAGCAACAAAATTTCAACAACTTTGACCTGTAACCAACCTTAATGTCTCAT 1022  
 DB 390 GTTGGAAATGAGGATTCATGAAGATCAAGAAATTCCAACTTGAATATCTTACAT 449  
 QY 1023 GTAGGAATGTCATGACCTGATCCCTGTGATCCCGTAAACTCATGGTATGATGAAC 1082  
 DB 450 GTTAAGAAACAGATTGATCTCATTAACCTTTACCAAGTGCTGTTGGGTAATGTAAT 509  
 QY 1083 ATAGGAATCGA 1093  
 DB 510 TCAGTATTTGA 520

RESULT 14  
 ID AAS20753 standard; DNA; 923 BP.  
 AC AAS20753;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Partial genomic DNA encoding part of tomato senescence-induced lipase.  
 XX  
 KW Plant; senescence-induced lipase; regulation of senescence;  
 KW environmental stress; tomato leaf; gene; ds.  
 XX  
 OS Lycopersicon esculentum.

XX Key Location/Qualifiers  
 FH exon 6..921  
 FT /\*tag= b  
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XX WO200198510-A2.  
 XX  
 PD 27-DEC-2001.



Db 676 CAGSGCGCAACTGATCGGCTACGTCGCCGTTTCCACCGACGAGACC CGCGCCTG 735  
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Db 736 GCGCGCGGACATCGCCATCGCTGCGCGGCGACGGTCAAGGAGCTCGAGTGGT 791

Search completed: December 26, 2005, 08:35:02  
Job time : 986.564 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 26, 2005, 07:08:48 ; Search time 8003.5 Seconds  
(without alignments)  
10916.277 Million cell updates/sec

Title: US-10-674-540A-1

Perfect score: 1537  
Sequence: 1 ggcacgagccatcccaaac.....ttagtttaaaaaaaaaa 1537

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_in: \*  
3: gb\_env: \*  
4: gb\_on: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pr: \*  
9: gb\_ro: \*  
10: gb\_sts: \*  
11: gb\_sy: \*  
12: gb\_un: \*  
13: gb\_vi: \*  
14: gb\_htg: \*  
15: gb\_pl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	1339.4	87.1	1341	15	AF026480 Arabidops
4	351.4	22.9	1239	6	AX507787 Sequence
5	351.4	22.9	1270	15	AY079356 Arabidops
6	351.4	22.9	1348	15	AY050998 Arabidops
7	291.2	18.9	1167	6	BD268758 DNA codin
8	291.2	18.9	1167	6	ARS76378 Sequence
9	255	16.6	96685	15	AC007087 Arabidops
10	255	16.6	115310	15	AC006931 Arabidops
11	180.2	11.7	1639	15	BT009343 Triticum
12	167.2	10.9	1805	15	AK098952 Oryza sat
13	165.6	10.8	1810	15	AK104373 Oryza sat
14	165.6	10.8	1810	15	AK106129 Oryza sat
15	165.6	10.8	1921	15	AK069577 Oryza sat
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17	165.6	10.8	110000	15	AP008207_295 Continuation (296
18	165.6	10.8	156850	15	AP002901 Oryza sat

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36	101.4	6.6	1400	15	AY085093 Arabidops
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#### ALIGNMENTS

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DEFINITION Sequence 1 from patent US 6774284.  
ACCESSION ARS76373  
VERSION ARS76373.1 GI:56578428  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 1537)  
Thompson, J.E., Wang, T.-W., Hudak, K. and Hong, Y.  
AUTHORS  
TITLE  
DNA encoding a plant lipase, transgenic plants and a method for  
controlling senescence in plants  
JOURNAL  
Patent: US 6774284-A 1 10-AUG-2004;  
Senesco, Inc.; New Brunswick, NJ  
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#### ORIGIN

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 DEFINITION DNA coding for plant lipase, transgenic plant and method for  
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 ACCESSION BD268753  
 VERSION BD268753.1 GI:33078521  
 KEYWORDS JP 2002536979-A/1.  
 SOURCE  
 ORGANISM  
 Dianthus caryophyllus (clove pink)  
 Dianthus caryophyllus  
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 Caryophyllales; Caryophyllaceae; Dianthus.  
 1 (bases 1 to 1537)  
 Thompson,J.E., Wang,T.W., Hudak,K. and Hong,Y.  
 DNA coding for plant lipase, transgenic plant and method for  
 controlling senescence of plant  
 Patent: JP 2002536979-A 1 05-NOV-2002;  
 SENESCO INC  
 OS Dianthus caryophyllus (carnation)  
 PN JP 2002536979-A/1  
 PD 05-NOV-2002  
 PR 14-FEB-2000 JP 2000599888  
 PI 16-FEB-1999 US 09/250280  
 PI JOHN E THOMPSON,TZANN WEI WANG,KATALIN HUDAK,YUMEN HONG PC  
 C12N15/09,A01H5/00,C12N1/21,C12N5/10,C12N9/20,C12N15/00,C12N5/10  
 CC DNA coding for plant lipase, transgenic plant and method for  
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 Best Local Similarity 99.9%; Pred. No. 4.3e-307;  
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 QY 121 CTTGGGCGGCGCTACTAAACCGGCTCAACATGAGCTCCGAGACTCTCTAGCGTGG 180  
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Qy	108	CTCGGGTCCAAATGCTTGGGCGGGCTACTAAACCGCTCAACGATGAGCTCCGTGAGCTC	167
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Qy	228	TGCGCTACTGCGGAGAGCGGCTACGAGGAGGCGACTTCAATTAAGACCGCTTC	287
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Qy	288	CCGGGGGCGGAGACCGGTTTGACGTGGTGGCTTGTACGCCACTGCGAAGGTCAAC	347
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Qy	588	GAAATGAGGAAAGAAAGCAATTCATTAATCAATGTTGTCGACTGTTTCAATTCAC	647
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Qy	1248	AATTAATCATGATGTTTCTTAAAGAAAGATTTGGTTCCTCAGCTTGATGGGTTGTG	1307
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VERSION			
AX507787.1 GI:23389024			
KEYWORDS			
SOURCE			
ORGANISM			
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Arabidopsis thaliana			
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
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Db	252	CGGCAAGCTGCTGTTTCTCTCCCGAAAGTTTGTCTTCCATTCATCAATTAAGAAATTC	311
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RESULT 5
LOCUS   AY079356               1270 bp    mRNA    linear    PLN 18-SEP-2002
DEFINITION   Arabidopsis thaliana putative lipase (At2g42690) mRNA, complete
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ACCESSION   AY079356
VERSION     AY079356.1
KEYWORDS    GI:19310712
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ORGANISM   Arabidopsis thaliana
REFERENCE   1 (bases 1 to 1270)
AUTHORS    Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Etgu,P.,
            Lee,J.M., Toriumi,M., Yu,G., Brooks,S., Chao,Q., Chen,H.,
            Karlin-Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M.,
            Palm,C.J., Shim,P., Southwick,A., Davis,R.W., Ecker,J.R. and
            Theologis,A.
TITLE       Arabidopsis Open Reading Frame (ORF) Clones
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 1270)
AUTHORS    Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,B., Dale,J.M.,
            Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
            Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
            Carlnici,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
            Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
            Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
            Sakurai,T., Satou,M., Seki,M., Shim,P., Southwick,A.,
            Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
TITLE       Direct Submission
JOURNAL    Submitted (19-FEB-2002) Plant Gene Expression Center, 800 Buchanan
            Street, Albany, CA 94710, USA
COMMENT     The RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAPL CDNAs (RAPL cDNA : 'RIKEN
            Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carlnici,P., Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PEGC (SSP) Consortium members constructed and
sequenced the pUNI (ORF) clones using the RAPL cDNAs: Yamada,K.,
Banh,J., Chan,M.M., Chang,C.H., Chang,B., Dale,J.M., Deng,J.M.,
Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,
Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H.,
Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J.,
Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shim,P.,
Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PEGC) and Seki,M. (RIKEN GSC) contributed equally
to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP
/PEGC) contributed equally to this work as p1s.

Annotation is based on the January 2002 version of the Arabidopsis
genome submitted to GenBank.
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ACCESSION AY050998.1 GI:15293128  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM Arabidopsis thaliana (thale cress)

REFERENCE  
 AUTHORS Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Ban, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinzaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.  
 Arabidopsis Full Length cDNA Clones

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS Arabidopsis Full Length cDNA Clones

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS Arabidopsis Full Length cDNA Clones

COMMENT  
 The Salk, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAPL cDNAs: Yamada, K., Liu, S.X., Pham, P.K., Ban, J., Banno, F., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koeseema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S.E., Shinzaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.  
 Direct Submission  
 Submitted (07-AUG-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA  
 RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs: 'RIKEN Arabidopsis Full-length cDNA': Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinzaki, K.

Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shim, P., Southwick, A., Tracy, S.E., Davis, R.W., Becker, J.R. and Theologis, A. Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

## FEATURES

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Matches 752; Conservative 0; Mismatches 466; Indels 81; Gaps 4;

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 Lin.X., Kaul.S., Shea.T.P., Fujii.C.Y., Shen.M., Vanaken.S.E., Barnstead.M.E., Mason.T.M., Bowman.C.L., Rensing.C.M., Benito.M.-I., Carrera.A.J., Creasy.T.H., Belli.C.R., Town.C.D., Nierman.W.C., Frazer.C.M. and Venter.J.C.  
 AUTHORS Unpublished  
 2 (bases 1 to 96685)  
 Lin.X.  
 JOURNAL Direct Submission  
 TITLE Submitted (09-MAR-2000) The Institute for Genomic Research, 9712  
 AUTHORS Medical Center Dr., Rockville, MD 20850, USA  
 REFERENCE 3 (bases 1 to 96685)  
 Town.C.D. and Kaul.S.  
 TITLE Direct Submission  
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 COMMENT On Apr 18, 2002 this sequence version replaced gi:6598662.  
 On Mar 7, 1999 this sequence version replaced gi:6151.  
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The annotation of this entry was produced with considerable contributions from Stephane Rombauts and Pierre Rouze, Department of Genetics, University of Ghent, Ledeganckstraat 35, 9000 Ghent, BE, E-mail: strom@genengp.rug.ac.be, piro@genengp.rug.ac.be A more detailed annotation of this entry and other sequences from the long arm of chromosome 4 can be viewed at: <http://webvr.mips.biochem.mpg.de/proj/thal/> this fragment has an overlap with ATAP22 at the 3 end.

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VERSION      AC006931.6
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ORGANISM      Arabidopsis thaliana
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AUTHORS      Barnes, M. E., Mason, T. M., Bowman, C. L., Romling, C. M.,
Benito, M., Carrera, A. J., Creasy, T. H., Buell, C. R., Town, C. D.,
Mierman, W. C., Fraser, C. M. and Venter, J. C.
JOURNAL      Unpublished
REFERENCE      2. (bases 1 to 115310)
AUTHORS      Lin, X.
JOURNAL      Direct Submission
REFERENCE      3. (bases 1 to 115310)
AUTHORS      Medical Center Dr., Rockville, MD 20850, USA
JOURNAL      Town, C.D. and Kaul, S.
REFERENCE      Direct Submission
AUTHORS      Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
JOURNAL      Medical Center Dr., Rockville, MD 20850, USA, cdtown@igr.org
REFERENCE      On Apr 18, 2002 this sequence version replaced gi:6598641.
AUTHORS      On Oct 8, 1997 this sequence version replaced gi:2443866.
JOURNAL      We have determined that YAC YUP812 is chimeric, and is comprised
REFERENCE      of two distinct genomic BcoRI fragments from chromosome I. This
AUTHORS      submission contains the sequence from the BcoRI site at position 1
COMMENT      (right end) to position 181918 of our previous Phase II
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ORGANISM    Triticum aestivum
REFERENCE   Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,
AUTHORS     Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
TITLE       Direct Submision
JOURNAL     Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
            Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
            USA
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Db      643 ACCGACGCGCTCGCCCTTCTCCAGTACAGCCGACGCACTGTGGCCACGCT- 701
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Qy      867 CTAGCCCGCAGACATCATAGTGTGAGCGCTTCGACATAGTGAATAATTCACCAACCGAG 926
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Qy      927 -----ATCCAGTACGCGCGTGTCTTCGGGTGCCAAAAGTGGCAAC 971
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Qy      1092 GAGCTGAGATGACCTGAGAGAGTCACTTTCTAA--GAACTGAAAAACCCGAGT 1148
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Db      1062 GACTACACAACCTGCGAGGAGTCTGCACGCTGCGGATGAAACGGGAGAGAGGC 1121
Qy      1209 GAGTTAAGGTTTGAATAAAGAGAGTGTGATTTGGTTAATAATGATGATTTTCTT 1268
Db      1122 GAGTTCAAGCTGCGAGTGAACCGGAGCGTGGCGCTGTGAAACAAGTGTCCGCTTCTC 1181
Qy      1269 AAGGAAGATGTTGTTCTTCCAGCTTGTGGTGTGCGAACAAGAGGATGTTTG 1328
Db      1182 AAGGATGACAACTCGTCCGAGAGTGTGGTGTGGAAGAAACAAGGGATGTGCTG 1241
Qy      1329 AATAAGATGTGTGATGTTTGGTCTCTCTTGAAGAA 1369
Db      1242 GGGCAACTGTGTGAGTGGAGCTGAGCAAGCCGCTGAGGA 1282

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DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J013055J12, full
            insert sequence.
ACCESSION  AK098952
VERSION     AK098952.1 GI:32984161
KEYWORDS    Oryza sativa (japonica cultivar-group)
SOURCE      FLI CDN; CAP trapper.
ORGANISM    Oryza sativa
REFERENCE   The Rice Full-Length cDNA Consortium, National Institute of
AUTHORS     Agrobiological Sciences Rice Full-Length cDNA Project Team,
            Kikuchi,S., Sato,K., Nagata,T., Kawagashira,N., Doi,K.,
            Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
            Kojima,K., Namiki,T., Ohneda,E., Yanagi,W., Suzuki,K., Li,C.,
            Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
            Science Genome Sequencing & Analysis Group, Otono,Y., Murakami,K.,
            Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
            Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
            Nariawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niihara,Y.,
            Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
            Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN,
            Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
            Hara,A., Hashidume,W., Hayatsu,N., Imocani,K., Ishii,Y., Itoh,M.,
            Kagawa,I., Kondo,S., Komoto,H., Miyazaki,A., Otsu,N., Ota,Y.,
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Best Local Similarity	54.6%;	Pred. No. 6.4e-24;		
Matches 368;	Conservative 0;	Mismatches 288;	Indels 18;	Gaps 1;

The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team: Kikuchi, S., Saech, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotte, I., Kojima, K., Namiki, Y., Ohneda, E., Taniguchi, M., Suzuki, K., Li, C., Ohtsuki, K., Shishikiri, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otsuno, Y., Murakami, K., Iida, Y., Sugano, S., Fujimatsu, T., Suzuki, Y., Tsunoda, Y., Kurokaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,





## ORGANISM

*Oryza sativa* (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS

The Rice Full-length cDNA Consortium, National Institute of  
Agrobiological Sciences Rice Full-length cDNA Project Team:  
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,  
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotte,I.,  
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,  
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International  
Science Genome Sequencing & Analysis Group, Otono,Y., Murakami,K.,  
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,  
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,  
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niihara,J.,  
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,  
Kusunegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:  
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,  
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,  
Kagawa,I., Kondo,S., Kono,H., Miyazaki,A., Oato,N., Oka,Y.,  
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,  
Yoshino,M. and Hayashizaki,Y.  
Collection, mapping, and annotation of over 28,000 cDNA clones from  
japonica rice  
Science 301 (5631), 376-379 (2003)  
12869764

TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

2 (bases 1 to 1921)  
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,  
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,  
Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hirooka,T.,  
Hori,F., Hotte,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K.,  
Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,  
Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M.,  
Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,  
Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Kono,H., Koyada,M.,  
Koya,S., Kurihara,C., Kurosaki,T., Kusunegi,T., Li,C., Lu,M.,  
Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A.,  
Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,  
Namiki,T., Narikawa,R., Niihara,J., Nishi,K., Nomura,K.,  
Numasaki,R., Ohneda,E., Otono,M., Ohtsuki,K., Oka,M., Ooka,H.,  
Oato,N., Oca,Y., Otono,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K.,  
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,  
Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S.,  
Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y.,  
Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,  
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,  
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and  
Yoshimura,A.  
Direct Submission  
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of  
Agrobiological Sciences, Department of Molecular Genetics, Head of  
Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki  
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,  
Tel:81-29-838-7007, Fax:81-29-838-7007)  
This clone is one of the 28k full-length cDNA clones from japonica  
rice.

## COMMENT

TITLE  
JOURNAL

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>  
NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K.,  
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,  
Ishikawa,M., Yamada,H., Ooka,H., Hotte,I., Kojima,K., Namiki,T.,  
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and  
Yamamoto,M.  
RIS Genome Sequencing & Analysis Group: Otono,Y., Iida,Y.,  
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,  
Kodama,T., Kurosaki,T., Kusunegi,T., Lu,M., Masuda,H., Miura,J.,  
Mizuno,K., Narikawa,R., Niihara,J., Oka,M., Ryu,R., Sugano,S.,  
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,  
Yoshimura,A., Matsubara,K. and Murakami,K.  
Genome Exploration Research Group in Riken Genomic Sciences Center  
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,  
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hangaki,T.,  
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,  
Hirooka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,

FEATURES  
SOURCE

Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,  
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Kono,H., Kouda,M.,  
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,  
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Oca,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,  
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,  
Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,  
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,  
Yasunishi,A. and Hayashizaki,Y.  
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Job time : 8013.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using bw model

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(without alignments)  
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Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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8: gb\_eest8.\*  
9: gb\_eest9.\*  
10: gb\_eest10.\*  
11: gb\_eest11.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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9	265.4	17.3	698	1	CD397937
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#### ALIGNMENTS

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DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone GS15T5L592D2 of Siliqua of strain col-0 of Arabidopsis thaliana (thale cress).

ACCESSION BX821625.1 GI:42468679  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Arabidopsis thaliana (thale cress)

#### REFERENCE

Castelli, V., Aury, J.M., Jallion, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

#### TITLE

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1270)

AUTHORS  
TITLE Direct Submission  
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage ; BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

#### COMMENT

The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction ; Temple G. Genoscope members carried out sequencing and annotation ; Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. UGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) . 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full length

http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=arabidopsis.  
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ORIGIN

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Best Local Similarity 57.6%; Pred. No. 2.8e-67;
Matches 749; Conservative 0; Mismatches 468; Indels 83; Gaps 6;

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Db 150 |CTTCGTCAACGACCAAACTCCAACTACTGTGAGCCGCGCTACGGCAAAATCTTCTTT 209
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Db 210 |CTTGACAGCAAG--GTCACTGCTGAAAAAGCTTCCGACTACGAGTGTGTAATCTTCTTA 266
Qy 329 |CGCCACTGCGAAGGTCAAGCTCCAGAGCGCTTCTGCTGAAGTCAAGTCAAGGAGAA 388
Db 267 |CGCCAGACGCTGCTGTTTCTCTCCCGAAG-TTGTGCTTCCCAATCAATCAAGAGATT 325
Qy 389 |GTGGATGAGGAATGGAATTGGATTGGGTATGTCTGTGTGCAATGACGAGAGTCG 448
Db 326 |TTGGACCGGTAGCTTAAGTGTGGCTTCACTGTCTCAAGTGTGATGAACGATCTAA 385
Qy 449 |GTGGCGGGGAGAGAGGTGATGTGTGAGAGAGGACTTGTAGAGATTATGATG 508
Db 386 |GGCTTTAGAGAGCGCCGTGAAACTATATGCTTTGAGAGAGAGAGAGAACTATGATG 445
Qy 509 |GGTGAATGTTCTGTGTGCTCAACTTGAAGTCTGCTCATCTTTGTTACGCACTCAACAAC 568
Db 446 |GATCAATGTTTGGGTGCTAGGCCCAACTTCAAGCTACCCCTTGTCAGCGACCGAGCA 505
Qy 569 |TACTCATGTGAAAAAGGTGAGAAATGAGAAAAAGAGCATTCATAATCAAGTTGTTGA 628
Db 506 |GGATGCTTCTGTGTGTGATGTTGA-----GGTA 534
Qy 629 |CGACTGTTCAAAATCAACTACTAGTTCCGCGTCCAAAAGCAAAAGAAAAAGAGAGCA 688
Db 535 |CGACTTT-----GATAGTGA 550
Qy 689 |CGACGACGATGATGACGACCCCAAGATGATGCAAGGTTG-ATGCAATATATACATCGG 747
Db 551 |CAGTGAATATGAAGAGGAGGTGAAGTATGATGCTGGGTGGCCTCAATATATATCTTGA 610
Qy 748 |AGGATCCCAATCACCTTTCACAAAACCTAAGTGCAGAAACACAACTTACAGACCAACTCA 807
Db 611 |ATCACCCCGGAATCGAAATTCATTAAGCTGAGCTTCAAGTGTGAGGCAAGATCA 670
Qy 808 |AAACAATAATGACAAATACAAAGAGCAAAACCTTAAGCATTAATTCGCGCGGTACAGCC 867
Db 671 |AGGAGCTTCTGTGAAGTATAGAGAGCAAGAAACGAGCAATGTGTGACTGAGCACTAGCT 730
Qy 868 |TAGGCGCAGACATACAGTGTGAGCGCTTTCGACATAGTGAGAA---TCTCAAGACCG 924
Db 731 |TGGGAGCTACAGAGGCTGTGTGGCGCTAGATATATAGCTGAGAAAGGTTCCAGTATG 790
Qy 925 |AGATCCCAAGTCAAGCGCGGTGTCTTGGGTGCTCCAAAAGTGAAGCAAAAATTCCAAC 984
Db 791 |ATGTTCCGCTCACTGTATAGTCTTTGGTGTTCACAGATGAGAAACAAAGGTTCAAG 850

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Qy 985 |AACTCTCGACTGCTGATCCCAACCTAAATGTCCTCCATGTGAAGAAATGTCATCGACTGA 1044
Db 851 |ACGAAGTAATGATGACGACAAAGACTTAAAGATCTCCATGTGAAGGACACGATTTGATCTCT 910
Qy 1045 |TCCCTCTGTATCCCGTAAACCTCAGTGGGTTACGGTAACATAGGAATGAGACTGGAGATCG 1104
Db 911 |TCATCTGATACCCAGGGGGGACTTTAGGTATGTGACATAGGAATTAATCTTTGTGATCG 970
Qy 1105 |ACTCGAAGAAAGTGCACCTTTCTAAAGACTCGAAAAACCCGAGTATGTCATTAATTTGC 1164
Db 971 |ATACAAAGAAAGTCAACCGTTCTCTTAAGCATTCAGAAATCCAGGGGATTTGGCATATTTCTTC 1030
Qy 1165 |AAGCAATATTCATGATGTTGAAGTGTGGCATGGGTTAAAGGGGAGTTTAAGTTGATTA 1224
Db 1031 |AGCGATGTTACATGTTGTAGCTGATGATGGAATGGGAAGAAAGAGATTAGACTGATGG 1090
Qy 1225 |ATAAGAAAGTGTGATGTTGTTAATATGATCTGATTTTCTTAAGAAAGAAATGTTGG 1284
Db 1091 |TTAAGAAAGATTTGCAATTGATGAACAATTCATGCGAGTTCTTGAAGCTGAGTGTGG 1150
Qy 1285 |TTCCTCAGCTGGTGGGTTGTGCAACAAAGGATGTTTGAATPAAGATGTGAGT 1344
Db 1151 |TGCCAGATCTTGTGTGGGTAGAGAAAGCAAGAGACTGATCAAGAACGAAGATGTGAT 1210
Qy 1345 |GGGTTTGGCTCTCTCTGAGGAAGATCTACTCTGAATT 1384
Db 1211 |GGGTTCTGCTCCGCTTGAAGAAAGACTGTATCTGAATT 1250

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RESULT 2
CN604658      661 bp      mRNA      linear      EST 10-MAY-2004
LOCUS        Vitis shuttleworthii L., grape Vitis shuttleworthii
DEFINITION   USDA_P1.131758 Vitis shuttleworthii L., grape Vitis shuttleworthii
cDNA clone MHV8015_E07 5', mRNA sequence.
ACCESSION   CN604658
VERSION     CN604658.1 GI:47090402
KEYWORDS    EST.
SOURCE      Vitis shuttleworthii
ORGANISM    Vitis shuttleworthii
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 661)
HUNTER, W., Dang, P., Chaparro, J., Lu, J. and Leong, S.
Expressed Genes in Vitis shuttleworthii L
Unpublished (2004)
Contact: Wayne Hunter, Phat Dang, USDA, ARS, Jiang Lu, FAMU
USDA-ARS, Horticultural Research Lab
U.S. Horticultural Research Lab
Ft. Pierce, FL 34945, USA
Tel: (772) 462-5898, (850) 412-7393
Fax: (772) 462-5986; (850) 561-2617
Email: whunter@usbrl.ars.usda.gov, pdang@usbrl.ars.usda.gov,
jiang.lu@famuc.edu
Seq primer: T3 Primer.
Location/Qualifiers
1..661
/organism="Vitis shuttleworthii"
/mol_type="mRNA"
/db_xref="taxon:246827"
/clone="MHV8015_E07"
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/tissue_type="Entire tendril, leaves, bud, flowers"
/dev_stage="at blooming"
/lab_host="X11-blue"
/clone_id="Vitis shuttleworthii L., grape"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; A high quality EST with at least 100 contiguous
bases at Trace Tuner score of 20 or better. Construction
by PM Dang, USDA, ARS, U.S. Horticultural Research Lab,
Ft. Pierce, FL, USA."

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ORIGIN



Query Match 19.2%; Score 295; DB 7; Length 661;  
 Best Local Similarity 66.6%; Pred. No. 5e-60;  
 Matches 440; Conservative 0; Mismatches 215; Indels 6; Gaps 1;

QY 715 TGATGCAAGTTGGATGACATATATACATCGAGGATCCCAATCACCCTTCAAAAC 774  
 DB 1 TCATGCGGGGTGGTTCACATCTACCTCAGGTGAGCCCAAGTCTTCAATTCACAAAG 60

QY 775 TAATGCAAGCAACCACTTCAGACCAACCAACCACTAATGACAAATATACAAAGC 834  
 DB 61 CAGAGCGCAAAACCACTTCATCAATCAATATTAACCTTGATGATATTAAGATTAAGACG 120

QY 835 AAACCCCTAAGCAATACATTCGCGGTCAAGCCTAGCGGACATATCACTCGTGAAGC 894  
 DB 121 AGAAGATGACATCATGTCACAGGTCAAGCCTGGGTGAGCTAGCAGATATGAGCT 180

QY 895 CTTTGCACATAGT-----GAGAAATCTACAGACCGAGATCCAGTCAAGGCGGTGCT 948  
 DB 181 CATTCGACATAGTATGAAAGAGATCGTCCCCCGATGTCATAGTATCAGCCATCGTCT 240

QY 949 TCGGTCGCCCAAGTAGGACCAAAATTTCCAAACCTTCGACTCGTACCCAAAC 1008  
 DB 241 TTGGTGTCCCGAAATGAGAACAGGCACTTCAATTAACAGATTAACCAACACTTCAAC 300

QY 1009 TAAATGCTCTCAATGTAAGGATGTCAATCGACTGATCCCTGTATCCGTAACCTCA 1068  
 DB 301 TCCACATCTCTCAATGTAAGGATGTCAATCGACTGATCCCTGTATCCGTAACCTCA 360

QY 1069 TGGGTTACGTGAACATAGAAATCGAGTGAATGATCGACTGAGGAAGTCACTTTCTAA 1128  
 DB 361 TCGGCTATGTGAAGACGGGAAGTGAATGATCGACTGAGGAAGTCACTTTCTAA 420

QY 1129 AGAAGCTGAAAAACCCAGATGTTGGCATATTTTTCGAAGCAATTTTCAGATTTGAAGT 1188  
 DB 421 AGAATTCGAAGAACCCGAGTGAATGTCGCAAACTTGAGGCAATGTCATGTCGTCG 480

QY 1189 GTTGCGCATGAGGAGTTAAGGAGTTTAAAGTTTGAATTAAGAAAGTGTTCATTGGTTA 1248  
 DB 481 GTTGCGCATGAGGAGTTAAGGAGTTTAAAGTTTGAATTAAGAAAGTGTTCATTGGTTA 540

QY 1249 ATAAAGTATGATTTTCTTAAGGAAGATTTTGTTCCTCAAGCTTGGGTTGTC 1308  
 DB 541 ACAAGTCTCTGTAATTTTCTCAAGGATGATGTCGTTGTTCCAGCTCATGGGTGAGGA 600

QY 1309 AGAACAAGGATGATTTTGAATTAAGATGATGATGATGATTTTGTTCCTCAAGGAAG 1368  
 DB 601 AGAACAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660

QY 1369 A.1369  
 DB 661 A.661

RESULT 3  
 CD860766/c 688 bp mRNA linear EST 11-JUL-2003  
 LOCUS TNE.002N24F011204 TNE Pisum sativum cDNA clone TNE002N24, mRNA  
 DEFINITION  
 ACCESSION CD860766  
 VERSION CD860766.1 GI:32544582  
 KEYWORDS EST.  
 SOURCE Pisum sativum (pea)  
 ORGANISM Pisum sativum  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;  
 Pisum.  
 1 (bases 1 to 688)  
 REFERENCE  
 AUTHORS Genoplatte.  
 TITLE Genoplatte, a major partnership french program in plant genomics  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Genoplatte  
 Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
 and <http://genoplatte-info.infodigen.fr>).  
 Location/Qualifiers  
 1..688  
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 /mol\_type="mRNA"  
 /cultiivar="Terese"  
 /db\_xref="taxon:3888"  
 /clone="TNE002N24"  
 /rissue\_type="scipule"  
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ORIGIN

Query Match 18.9%; Score 290; DB 6; Length 688;  
 Best Local Similarity 65.2%; Pred. No. 8.1e-59;  
 Matches 442; Conservative 0; Mismatches 235; Indels 1; Gaps 1;

QY 688 AGACGACGATGATGACGACCCCAAGTATGACAGGTTGATGACATATACATCGG 747  
 DB 687 ATGAGATGACCAAGGCTCCGAAAGTATGAAAGGTTGCTGACCATATACCTCAG 628

QY 748 AGATCCCAATACACCTTCAAAAATAAGTCAAGAACACAACTTCAGACCAACTCA 807  
 DB 627 ACACCAAAATCTCTTTCATCTAAACAGCGGTGATCCAGATCTTAACAAAGTAA 568

QY 808 AACCACTAATGACAAATATACAAAGACGAACCTTAAGCATTAATTCGCGGTACAGCC 867  
 DB 567 AAAGTTGTTGAACATTTTACAGAAATGAATCCAGTGTGATGATGTCGAGACACAGTC 508

QY 868 TAGCGGACATATCATGTGTGAGCGCTTTCACATAGTGAAGATCTCAGACGAGA 927  
 DB 507 TAGAGC-AGTCTATCATGTTGATGTCGTTTGAATTTGTCGAATGATGTAACAGCA 449

QY 928 TCCAGTCAAGCGCGGTCTTCGCGTCCCAAAAGTAGGCAACAAAATTTCCAAAC 987  
 DB 448 TTCCCGTGAAGCTTTGTGTTGTTGTTGCCCAAGTGTGGAAACAAAGCATTCATGACA 389

QY 988 TCTTCGACTGTATCCCAACCTTAATGTCTCTCATGTGAAGATGTGATGACTGATTC 1047  
 DB 388 GGTTCAAAAGTTTCCGAATTTGAAGGTGTTACGAGGAATGTGATGATCTTATAC 329

QY 1048 CTCTGTATCCCGTGAACCTATGAGTGTACGTGAACATAGGAATGACTGAGATCGACT 1107  
 DB 328 CGCATTAATCCAGGAAGTTATTTGGGATATGATATACAGGTGTATGATGTTGATTAACA 269

QY 1108 CGAAGATGACCTTTCTAAGGACTCGAAAAACCCAGATGATGATTAATTTGCAAG 1167  
 DB 268 CAGGAATATCAAGAGTTTGAATGATTCGAAAGATCCGAGTATGATTAATTTGCAAG 209

QY 1168 CAATATTGATGTTGTAAGTGTGTCATGAGGTTAAGGAGGATTTAAGTTGTAATA 1227  
 DB 208 CTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 149

QY 1228 AGAAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1287  
 DB 148 AGAAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 89

QY 1288 CTCAGCTGTGAGGTTGTCAGAACAAAGGATGTTTGAATTAAGATGATGATGATGATGATGATGAT 1347  
 DB 88 CAGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 29

QY 1348 TTTTGTCTCTCTGAGG 1365  
 DB 28 TTGATGATCCTGCGCGG 11

RESULT 4  
 AM132739/c 621 bp mRNA linear EST 08-JUL-2004  
 LOCUS AM132739

DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
seq96910.y1 Gm-cl013 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl013-3043 5' similar to TR:Q9ZTW1 Q9ZTW1 LIPASE ;, mRNA sequence.	AW132739	AW132739.1	GI:6134346	EST.	Glycine max (soybean)	1 (bases 1 to 621)	Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marras, M., Hillier, L., Kueba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Pearson, B., Swallow, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Rittler, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materon, R. and Wilson, R.	Public Soybean EST Project	Unpublished (1999)	Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. Possible reversed clone: similarity on wrong strand This clone is available through: Biogenetic Services, 801 32nd Ave, Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Seq primer: -40RP from Gibco High quality sequence stop: 407.						location/Qualifiers				
1..621						/organism="Glycine max"				
/mol_type="mRNA"						/cultivar="Williams"				
/db_xref="taxon:3847"						/clone="GENOME SYSTEMS CLONE ID: Gm-cl013-3043"				
/tissue_type="whole seedlings, 2-3 week old seedlings, greenhouse grown"						/lab_host="XL10-Gold"				
/clone_1ib="Gm-cl013"						/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI. This cDNA library was constructed from mRNA isolated from whole seedlings of 2-3 week old greenhouse grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."				
ORIGIN										
Query Match	18.5%;	Score 283.6;	DB 1;	Length 621;						
Best Local Similarity	66.6%;	Pred. No. 2.8e-57;								
Matches 403;	Conservative 0;	Mismatches 202;	Indels 0;	Gaps 0;						
783	AGAACACAATTGCGCGGTACAGCCTTAACTCAACAACTAATGACAAATACAAAGACCAACCTTA	842								
DB	621	AGGACGCGAGTTTCAAGACCCACGTCAAAATCCCTTTACACCAATTACAGCTTTGAGACCCCA	562							
QY	843	AGCATTAACATTGGCCGCTACAGCCTTAAAGCGGACACATCATGCTGAGCGCCCTTTCAC	902							
QY	561	GCTTTGTCATCTGTGGGGGACAGCCTTGGCGGACACCTATCATGCTGAGCGCCCTTTCAC	502							

DB	QY	LOCUS	DEFINITION	ACCESSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
QY	903	ATAGTGGAGATCTCAGACCGAGATCCCATGCGGCGCTTGCTTTCGGGTGCCCAAA	962	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
Db	501	CTGTCGAAAAACGGGGTAAACGAGTCCCGGTACAGGCTGATGCTTCCCGGATG	442	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
QY	963	GTAAGCAACAAAAATTCCAAACAATCTTGACTGTACCCAAACCTTAAATGTCCTCAT	1022	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
Db	441	GTCCGAAACAAGGCTTCAACGAGAGGTCAACATGTTCCGAACCTTGAAGTTTTCAC	382	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
QY	1023	GTAAGAAATGTCATCGACCTGATTCCTCTGTATTCCTCGTAAACATCAGGGTATAGTAAC	1082	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
Db	381	GTGAAGAACGGATCGATTGATCCACACTACCCGGGGAAGTTGTAAGGTATAGATAC	322	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
QY	1083	ATAGAAATTCAGCTCGAGATCGACTCGAGAAAGTCACCTTTCTTAAGSACTCGAAAAAC	1142	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
Db	321	ATGGCACACGAGCTGTGTATGACACAGAGAGTCCGAGCTTGAAGAGATCGAAGAAC	262	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
QY	1143	CCGAGTATTTGGCAATTTTGCACAAATATTGCATTTGTAAAGTGTGGCATGGGGTT	1202	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
Db	261	CCGGGTATTTGGCAATTTTGCACAAATATTGCATTTGTAAAGTGTGGCATGGGGTT	202	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
QY	1203	AAGGGGAGTTTAAGTTTGAATTAAGAAAGTGTGCATTTGTTAATTAATCATGTGAT	1282	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
Db	201	AAGAGAGATTTTGAATTAAGTAAAGAGAGTGTGCGTTGGTGAATTAAGTCTGTGAG	142	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
QY	1263	TTTCTTAAGAGAAATGTTGGTCTTCCTCAGCTGTGGGGTGTGCGAACAAGGGATG	1322	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
Db	141	TTTCTTAAGAGAAATGTTGGTCTTCCTCAGCTGTGGGGTGTGCGAACAAGGGATG	82	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
QY	1323	GTTTTGAATAAGATGTGAGTGGGTTTGGCTCTCTGAGAAAGATCTTACTCTGAA	1382	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
Db	81	GTGAAGAGGAGAGATGGGAGTGGGTGTGATGTCGCAAGTGAAGAGATGTGCTGTG	22	BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
QY	1383	TTTGA 1387		BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				
Db	21	CTCGA 17		BG321342	898 bp	mRNA	linear	EST 27-FEB-2001				

RESULTS

LOCUS

DEFINITION

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

898 bp mRNA linear EST 27-FEB-2001

D801\_07e07 A D801 AAF C ECOR C cold stressed Flaxseed seedlings

Descourainia sophia cDNA clone D801\_07e07, mRNA sequence.

BG321342

BG321342.1 GI:13151020

EST.

Descourainia sophia

Descourainia sophia

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Descourainia.

1 (bases 1 to 898)

Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Onelliet,T., Robert,L.S., Sprout,D. and Tinker,N.A.

Expressed Sequence Tags from Cold-Stressed Descourainia sophia Seedlings

Unpublished (2001)

Contact: Singh,J.A.

Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-food Canada

KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A 0C6, Canada

Tel: (613) 759-1662

Fax: (613) 759-1701

Email: singhja@agr.gc.ca.

location/Qualifiers

1..898

/organism="Descourainia sophia"

/mol\_type="mRNA"

/db\_xref="taxon:89411"

/clone="D801\_07e07"

/rfeature\_type="leaf, stem"

/dev\_stage="1-month seedlings - 1 cm tall - 8 leaf"



RESULT	7
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LOCUS	684 bp mRNA linear EST 12-DEC-2000
DEFINITION	MCTO26G05.171831 Ice plant Lambda uni-zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCTO26G05 5,
ACCESSION	CAB839368
VERSION	CAB839368.1 GI:26567133
KEYWORDS	EST.
SOURCE ORGANISM	Mesembryanthemum crystallinum (common iceplant)
REFERENCE	Mesembryanthemum crystallinum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum. 1 (bases 1 to 684) Cushman, J.C. An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum Unpublished (1997) Contact: Cushman JC Department of Biochemistry University of Nevada MS200, Reno, NV 89557-0014, USA Tel: 775-784-1918 Fax: 775-784-1650 Email: jcushman@unr.edu PCR Primers FORWARD: T3 20mer BACKWARD: T7 21mer Plate: 026 row: G column: 05 Seq primer: T3 20mer High quality sequence stop: 684.
JOURNAL COMMENT	
FEATURES	location/Qualifiers 1..684 /organism="Mesembryanthemum crystallinum" /mol_type="mRNA" /db_xref="taxon:3544" clone="MCTO26G05" /tissue_type="leaf" /dev_stage="five-week-old" (clone_lib="Ice plant Lambda uni-zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM))."
SOURCE	

Query Match	17.7%	Score 273.4	DB 6	Length 684
Best Local Similarity	67.8%	Pred. No. 1.4e-54		
Matches 381	0	Mismatches 181	Indels 0	Gaps 0

QY	28	CCACTCAAAACTATATCCAA	CTGGCTGCAGAAAGCCCAAC	CTTTAAGGCTCTCAAAAGCCG	87
Db	16	CACCAAAACACACCTCTAC	ATGAACAATGGCCCAACAACT	CGGGAAGGAGGCGG	75
QY	88	GCCCAACATGGCCCGAACT	CTCTGGGATCCAATGCTTGGCCG	GGCTACTAAACCCGCTCA	147
Db	76	GCCCCATATGGCAACGACT	CTTAGGAAAACTCATGGATGGCT	ATTTGAACCCACTTAA	135
QY	148	ACGATGAGCTCCGTGAGCT	CCTCTAGGCTGCGGGACCTT	CTGGCAGTGAATATACGA	207
Db	136	ACTATGATCTCCGTGCTG	ATCTCCGTGTGTGTGACCTA	TGTGCAGGTCCTACGACA	195
QY	208	CCTTCATPAAACGACAGAA	CTGATCTACTGCGGACAGCC	CGCTACGGGAAGGCGGAC	267
Db	196	CGTTCACTAACGACCCCA	CTCCGAGTACTGCGGCTCA	CGCCGCTTACGCCAAGCCG	255
QY	268	TACTTCATPAAACCGCCTT	CCCGGGGAGGCGCAGAC	CGGTTTGAACGTGGTGGCTA	327
Db	256	TCCTCGAACAAACCGCCTT	CCCTGTGTGGCGGCGCGCTA	CGATGGGATTTCTCAT	315
QY	328	AGCCCACTGCGAAGCTCAG	CGCTCCCAAGGCGTTTCTG	CTGAATCCAGCTCGAGGGA	387
Db	316	ACGCTACCGCGAGAGTG	ATGATACGCGCAAGGCTTTG	TTCATTAACTACCGCTCGG	375
QY	388	AGTGGGATPAGGGAATCGA	TTGGAATGGGGTATGTCGTG	GTCTCGAATGACGACGATC	447
Db	376	TGTGGGACAAAGAGTCA	ATGGAATGGGATATGTTCTT	GTACGAAATGATAGCGCA	435
QY	448	GGGTGGCGGAGCGAAGG	AGGTGATGTGTGTGAGAGG	GAAGGACTTGTAGGGATTAT	507
Db	436	CGAGATATGGGAGGAGAG	AGATTATATGTGGGTGAGAG	GGGACTTACGAGATATTAG	495
QY	508	GAGTTGATGTTCTTGTG	ATCTCACTTGAGTGTGCTAT	CCTTTGTGTACGCACTCA	567
Db	496	GGGTTGATGTCTTGAG	CGCTTCGTTGAATCTGCT	GAACCTCTCGTTTGTGA	555
QY	568	CTACTCATGTTGAAAAG	STGGA 589		
Db	556	GTTCTGTGTCAGAGATGA	AGA 577		

RESULT 8	CD397937/c	707 bp	mRNA	linear	EST 07-JUN-2003
LOCUS	Gm_CK18965	Soybean induced by Salicylic Acid	Glycine max	cDNA 3'	
DEFINITION	mRNA sequence.				
ACCESSION	CD397937				
VERSION	CD397937.1	GI:31455909			
KEYWORDS	EST.				
SOURCE	Glycine max (soybean)				
ORGANISM	Glycine max				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.				
AUTHORS	1 (bases 1 to 707) Tian,A.G., Wang,J., Cui,P., Han,Y.J., Xu,H., Cong,L.J., Huang,X.G., Wang,X.L., Jiao,Y.Z., Wang,B.J., Wang,Y.J., Zhang,J.S. and Chen,S.Y.				
TITLE	Characterization of soybean genomic features by analysis of its expressed sequence tags				
JOURNAL	Theor. Appl. Genet. 108 (5), 903-913 (2004)				
PIUMED	14624337				

COMMENT Contact: Chen S-Y  
Plant Biotechnology Laboratory  
Institute of Genetics and Developmental Biology, CAS, China  
Datun road, Beijing 100101, China  
Tel: 86-10-64886859  
Fax: 86-10-64873428  
Email: sychen@genetics.ac.cn  
Email: sychen@genetics.ac.cn  
Seq primer: T7 primer.  
Location/Qualifiers  
1. .707  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Kefeng 1"  
/db\_xref="taxon:3847"  
/tissue\_type="Seedlings"  
/dev\_stage="two-week seedlings"  
/lab\_host="X11-Blue MRP strain"  
/clone\_id="Soybean induced by Salicylic Acid"  
/note="Vector: pBluescript SK+; Site 1: EcoR I; Site 2: Xho I; The cDNA library was constructed by He, C-Y from mRNA isolated from two-week seedlings (cultivar Kefeng 1) treated by spraying 2.0mM salicylic acid for 24, 36, 48 and 72 h. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(AT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into X11-Blue MRP host cells (Stratagene)."

ORIGIN  
Query Match 17.6%; Score 271; DB 6; Length 707;  
Best Local Similarity 63.7%; Pred. No. 3.1e-54;  
Matches 431; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

QY 858 GGTGACAGCCGAGCGGACACTATCAGTCGCGCTTGCACATAGTGAAGATCTC 917  
DB 707 GGGGACAGCCCTCGGCGGACCTTATCCATCGTAGCGCTTGCACCTGTTGAAACGGG 648  
QY 918 ACGACCGAGATCCGAGTCACGCGCGTGTCTCCGGTCCCAAGTAGAGCAACAAAA 977  
DB 647 GTACGAGAGTCCCGTTACCGCATGTGTTCGGGTCCCGCAGTCCGAAACAGGCC 588  
QY 978 TTCCAAACAATCTTTCGACTGTACCCAACTAAATGCTCTCCATGTAAAGATGTATC 1037  
DB 587 TTCAACGAGAGTTCGACATGTTCGAACTTGAAGTTTGCACGTGAAGACGTATC 528  
QY 1038 GACCTGATCCCTCTGTATCCCGTGAATCAATGGTTACGTGAAGATGAAGTGC 1097  
DB 527 GATTGTATCCCACTACCTCCGGGAAAGTTTAAAGTAGTACATAGGACGAGATG 468  
QY 1098 GAGATCACTGAGGAAGTGCACCTTTCTAAAGACTGCAAAACCCGAGTATGGCAT 1157  
DB 467 GTGATACACGAGAAATGCGCCGAGCTTGAAGACTGCAAGAACCCGCGTATGGCAT 408  
QY 1158 AATTGCAAGCAATATTCATGTGTAAAGTGTGGCATGGGGTTAAAGGGAGTTAAG 1217  
DB 407 AACTTGCACGAGATGTTCATGTGTGGCGGGTGAATGGAAGAAAGAGAGATTGAG 348  
QY 1218 GTTCTAAATAGAGAAAGTGTTCATGTGTAAAGTCAATGTTTCTTAAAGAAAG 1277  
DB 347 ATGAGGAGTGAAGAGAGTGTGTGTGTGTAAAGTGTGTGTGTCTTAAAGAGAA 288  
QY 1278 TGTGTGTTCTTCAGCTGTGTGTGTGTGTGCAAAACAAAGGATGTTTGAATTAAGAT 1337  
DB 287 TATGCGGTGCAAGGAGTGTGTGTGTGTGTGAAGAAATAGGGAGTGTGAAGAGGAGAT 228  
QY 1338 GGTGAGTGGGTTTGGTCTCTCTGAGAGAGATCTTCTGAATTGA-----TTGA 1391  
DB 227 GGGGAGTGGGTTGATGCGCCAGATGAGAGATGTGCTGTGCTGAAGAGATTGA 168

QY 1392 TAAATTTTCATCAGTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTATG 1451  
DB 167 TTAGCTTAAGCTTGCATAGTAGAGACTGTTAATCTTCACTATGATGAAACATTATTC 108  
QY 1452 GGACTAAGTACTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1511  
DB 107 AATCTTAATCTTCTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 48  
QY 1512 TTGCATTTAGTTTAA 1528  
DB 47 ATATATTTTATGTTTAA 31

RESULT 9  
AV784335/c 698 bp mRNA linear EST 28-MAR-2002  
LOCUS AV784335 RALV5 Arabidopsis thaliana cDNA clone RALV5-18-J03 3',  
DEFINITION mRNA sequence.  
ACCESSION AV784335 GI:19803125  
VERSION AV784335  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 698)  
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
Aizawa, T., Shibata, K., Shingawa, A., Muramatsu, M., Hayashizaki, Y.  
and Shinozaki, K.  
Large scale analysis of Arabidopsis full-length cDNA (2002b)  
Unpublished (2002)  
TITLE Contact: Motoaki Seki  
JOURNAL Plant Functional Genomics Research Group  
COMMENT RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: msek@rcc.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially  
as reported previously (Seki et al., 1998). This clone is in a  
modified pBluescript vector as a Set1/XhoI insert. Please visit our  
web site ([http://www.gsc.riken.go.jp/e/Plant/index\\_e.html](http://www.gsc.riken.go.jp/e/Plant/index_e.html)) for  
further details.

FEATURES  
source Location/Qualifiers  
1. .698  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/db\_xref="taxon:3702"  
/clone="RALV5-18-J03"  
/dev\_stage="Rosette plants"  
/lab\_host="SOLR"  
/clone\_id="RALV5"  
/note="Site 1: Set1; Site 2: XhoI; subjected to  
dehydration-reated(1,2,5,10,24 hr)"

ORIGIN  
Query Match 17.3%; Score 265.4; DB 1; Length 698;  
Best Local Similarity 64.7%; Pred. No. 7e-53;  
Matches 411; Conservative 0; Mismatches 221; Indels 3; Gaps 1;

QY 753 CCCAATCACCCCTTCAACAACTAATGCAAGAACACACTTCAAGACCAACTAAACA 812  
DB 697 CCCGAATCGAAATTCATTAAGTCTACGCTGACAGTTGTTAGCCAAAGATCAAGAG 638  
QY 813 CTAATGACAAATATCAAGAGCAAAACCTAAGCATTAATTCGCGGTCAAGCTAGGC 872  
DB 637 CTTCTGTGAAGTATTAAGACGAGAAACGAGCATTTGTGATGACATAGCTTGGGA 578  
QY 873 GCGACACTATCAGTGTGAGCGCTTGCACATAGTGAAGAA---TTCACAGACCGAGATC 929  
DB 577 GCTACAGAGGCTGTTTGGCGCGCTTATGATATAGCTGAGAAAGGTTCCAGTATGATGTT 518

QY	930	CCAGCAACGGCCGGGCTCTTGCGGGGCCCAAAAGTAGGCACAAAAAATTCACCAACTC	989
Db	517	CCGGTCACTGCTATAGTCTTTGGTTGTGCCACAGTAGAAMACAGAGATTCAAGAGCAAA	458
QY	990	TTGCAGCTGTACCCAAACCTAATATGTCTCCATGTAGAAATGTCAATCGACTGATCCCT	1049
Db	457	GTAATGAGATCAAAAGAACCTTAAGATCCTCCATGTAAAGAAACACGATTGATCTCTTAAC	398
QY	1050	CTGATATCCCGAAGAACTCATGGGTATAGTGAACATAGGAATCGAGCTGAGATCGACTCG	1109
Db	397	CGATATCCAGGGGACCTTTTAGGGTATGTGGACATAGGAATTAACCTTTGTATGATACA	338
QY	1110	AGGAAGTCGACCTTTCTTAAGAGACTCGAAAAACCCGAGTGAATGGCATTAATTTGCAACA	1165
Db	337	AAGAAAGTCACGGTCTCTTAAGGCAATTCAGAGAAATCGAGGGGATTTGGCATTAATCTTCAGCG	278
QY	1170	ATATTGCATTTTGTAAAGTGTGTGCAATGGGGTTAAGGGGCACTTAAAGTTGTAAATAG	1229
Db	277	ATGTTACATGTTGTATGCTGGATGTGAATGGGAAGAAAGATTTAACTGATGTGTAAAG	218
QY	1230	AGAGTGTGTCATTGGTAAATTAAGCATGTGATTTTCTTAAGGAAGAAATGTTGGTCT	1289
Db	217	AGAAATATTGCATTATGTGAACAGTCAATGCAAGTCTTTGAAGCTGAAATGTTTGGTGC	158
QY	1290	CCAGCTTGTGGGTGTGCAGAACAAAGGATGTTTGAATTAAGATGTGAGTGGGT	1349
Db	157	GGATCTTGTGGTGTGAGAGAAAGAAACAAAGACATGATCAAGAACGAAGATGTGAATGGGTT	98
QY	1350	TTGGCTCTCCGAGAGAAAGATCTTACTCTGAAT	1384
Db	97	CTTGCTCCCGTTGAGAAAGAACTGTACTGAAAT	63

JOURNAL  
COMMENT  
Unpublished (2004)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr  
The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out  
full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli  
V., Aury J.M., Taillon O., Winkler P., Nenard M., Crnaud C.,  
Schachter V., Weissenbach J., Salanoubat M.  
URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis  
genome released by MIPS (Munich Information center for Protein  
Sequences).  
[http://www.genoscope.cns.fr/externe/sequences/Banque\\_Projet\\_BF\\_EST](http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF_EST)  
<http://www.genoscope.cns.fr/cgi-bin/g9b/g9b?source=Arabidopsis>.  
Location/Qualifiers  
1. .686

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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecolytpe="Col-0"
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/clone_id="Arabidopsis thaliana Adult vegetative tissue
Col-0"

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	Query Match	Best Local Match	Similarity	16.7%;	Score	256.2; DB	5;	Length	686;	
	Matches	420;	Conservative	0;	Mismatches	233;	Indels	4;	Gaps	2;
QY	732	ACATATATACATCGAGGATCCCAATCAACCTTCACAAAACTAAGTCAGACACAA	791							
DB	686	ACATCTATAGTAGTAATCAACCCCTAATCTAAATTCCTAAGCTGAGTCAACGGTCACAG	627							
QY	792	CTTCAGACCAAACTCAAACTAATATGACAAATATCAAAAGCGAAACCTTAAGATTAACA	851							
DB	626	TTGTATGCCAAGATCAAGAGCTTCCTGTGAAGTATAGGACGGAACCGAGAAATGGTT	567							
QY	852	TTGCCCGCTCAGACGCTTGAAGCGGGAACATATCATGTGTGAAGCGCCCTTCACATATGGGA	910							
DB	566	GTATACCTGGAATATGCTTGGAGCTTAACAGAGCTGTTCTGGCGCCCTATATGATATAGCTGA	507							
QY	911	GAA---TCTCCAGACCGAGATCCCACTCAGACGCGCCGCTGCTTCGGAGTCCCAAAAGTAGG	967							
DB	506	GAAACGTTCCAGTATATATGTTCCGGTCACTGCTATATGTTCTTGGTTGTCCACAGTAGG	447							
QY	968	CACAAAAAATTCACACACTCTTCGATCGATCCCAACCTAAATGTCTCATGTAAAG	1027							
DB	446	AAACAGAGAGTTCAAGACGAAAGTAATGATCAACAAGACTTAAGATCCTCATGTAAAG	387							
QY	1028	GAATGTATCGACCTGATCCCTCTGTATCCCGTAAACTCATGGGTTATAGTAAACATAGG	1087							
DB	386	GAAACAGATGATCTTAACTCATACCCAGCGGAGCTCTTAAGGATATGTGGACATAGG	327							
QY	1088	AATCAGAGCTGAGATTCGACTCGAGAGATCGACCTTTCTAAGGACTCGAAAAACCCGAG	1147							
DB	326	AATAAACTTGTGATCGATACAAAGAAAGTCAACGTTCTTAAAGCAATTCAGAAATCCAGG	267							
QY	1148	TGATTTGCAATATTGCAAGCAATATTGCAATGTTGAATGTTGGCATGGGTTAAAGG	1207							
DB	266	GGATTTGGCATATCTTCAGGCGAGATCTTACATGTTGTACTCGAGATGGAATGGGAAGAAAG	207							
QY	1208	GGAGTTTAAGGTTGTAAATAAGAGAGTGTTCATGTTGTTAATAATGATCATGTAATTTCT	1267							
DB	206	AGAGCTTAACTGATGTTTAAGAGAAATGATTCATATGTAACAAGTCATCCGAGTTCTT	147							
QY	1268	TAAAGAGAAATGTTTGGTTCTCTCCAGCTTGGTGGGTTGTGCAAAACAAGGAAATGGTTT	1327							
DB	146	GAAAGCTGAGTGTGTTGGTCCAGAGATCTTGATGGGTAGAGAAACAAGAGATCGATCA	87							
QY	1328	GAATTAAGAGATGATAGTGGGTTTGGTCCCTCCGAGGAAAGATCCTCATCTGTAAT	1384							
DB	86	GAACGAATATGTAAATGGGTTCTCGCTCCGCTTGAAGAAACCTGTACTGTAAT	30							

RESULT 11				
LOCUS	AM774539/c			
DEFINITION	AM774539	648 bp	mRNA	linear
ACCESSION	EST333690	KV3	Medicago truncatula	cDNA clone pKV3-22U18, mRNA
VERSION	sequence.			
KEYWORDS	AM774539			
SOURCE	AM774539.1	GI:7718456		
ORGANISM	EST.			
	Medicago truncatula	(barrel medic)		
	Medicago truncatula			
	Eukaryota; Viridiplantae;	Streptophyta;	Embryophyta;	Tracheophyta;
	Spermatophyta; Magnoliophyta;	eudicotyledons; core eudicotyledons;		
	rosids; eurosids I; Fabales;	Fabaceae;	Papilionoideae;	Trifoliaceae;
	Medicago.			





fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."

## ORIGIN

Query Match 16.2%; Score 248.4; DB 2; Length 623;  
Best Local Similarity 66.0%; Pred. No. 8.8e-49;  
Matches 406; Conservative 0; Mismatches 202; Indels 7; Gaps 3;

Qy 749 GATATCCCAATACACCTTTCACAAATAGTGAAGAACACAACTTCAGACCAACTCA 808  
Db 612 GCACCAAAAATCCTCTTTCATCCATCCAGGCAAGAACGACGTTCAAGCCCACTCAA 553  
Qy 809 ACAACTAATGACAAATTCAGAAAGCAAACTTAAGCTTAACATTTCCCGGTCAAGCT 868  
Db 552 TCCCTCTA---CAACATTACAGCTCTGAGAACCCAGCTTGTTCATCTGTGGGACAGCAT 496  
Qy 869 AGGGGCGACATATCAGTCGTGAGGCGCTTGACATATGTGAGAACTCAGACCGAGAT 928  
Db 495 CGGGGCAACCTATTCATCTGAGGCGCTTGACATCTGTCGAAACGCGGTAAAGAGAT 436  
Qy 929 CCCAGTCAGGCGCGTGTCTTCGGGTGCCCAAAAGTACGCAACAAATTCACAACT 988  
Db 435 CCCGTCACCGGCATCTGTCTCGGGTCCCGCAGGTGCAAAACAGGCTTCAACGAGAG 376  
Qy 989 CTTCGACTCTGATCCCAAACTTAATGTCTTCATGTAAGAAATGTCATGACCTGATCCC 1048  
Db 375 GTTCACATCTGTTCCGAACCTGAAGTTTTCACGTGAAGAACGTGATCGATTGATCCC 316  
Qy 1049 TCTGTATCCCGTGAACATCATGAGGTAGTGAATAGAAATCGAGCTGAGATGATC 1108  
Db 315 ACATACCCGGGAAAGTTGTTAGGTATGATGACGCGACGAGCTGTGATAGACAC 256  
Qy 1109 GAGGAAGTCGACCTTCTTAAGAAGACTCGAAACCCGAGTATGTCATTAATTTGCAAGC 1168  
Db 255 GAGGAAGTCGCGGAGCTTGAAGAGACTCGAAGAACCCGGGTATTTGGCATTACTTGCAAGC 196  
Qy 1169 -AATATTGATGTTG--TAAGTGTGGCATGGGGTTAAGGGGAGATTAAAGTTGTA 1224  
Db 195 GNATGTTCATTTGGGTGGCGGGGTGGAATGGGAAGAGAGAGATTATGATGAGG 136  
Qy 1225 ATAAGAAAGTGTTCATTTGTTAATAGTATGATGATTTCTTAAGGAAGAAGTTGG 1284  
Db 135 TGAAGAGAGAGTGGCGGTGGTAATAGCTTGTGAAGAGAGAAATATGGCG 76  
Qy 1285 TTCCCTCAGCTTGGTGGTGTGTCAGAAACAAAGGATGTTTGAATAGATGGTGAAGT 1344  
Db 75 TGCCAGGGTCTGTGGTGGTGAAGAAATTAAGGGATCTGTAAGAGGAGATGGGAGT 16  
Qy 1345 GGGTTTGGCTCTC 1359  
Db 15 GGGTGTGGATGGCG 1

RESULT 13  
CV708865/c 744 bp mRNA linear EST 03-NOV-2004  
LOCUS UCRPT01.0011p17.f Poncirus trifoliata CTv-challenged cDNA library -  
DEFINITION AG12 Poncirus trifoliata cDNA clone PT\_68A0011p17, mRNA sequence.  
ACCESSION CV708865  
VERSION CV708865.1 GI:55291233  
KEYWORDS EST.  
SOURCE Poncirus trifoliata  
ORGANISM Poncirus trifoliata  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Sapindales; Rutaceae; Poncirus.  
REFERENCE 1 (bases 1 to 744)  
Roose, M.L., Ye, X., Federici, C.F., Close, T.J., Fenton, R.D.,  
AUTHORS Manamaker, S., Kim, H.R., Kudrna, D. and Stum, D., Misoetski, M.,

TITLE  
JOURNAL  
COMMENT  
wings, R.  
Development of EST Resources and New Genetic Markers for California  
Citrus - Poncirus trifoliata CTv-challenged phloem - AG12  
Unpublished (2004)  
Contact: Mikeal Roose  
Department of Botany & Plant Sciences, University of California  
Riverside, CA, 92521-0124, USA  
Tel: 9097874137  
Fax: 9097874437  
Email: mikeal.roose@ucr.edu  
Seq primer: T7

## FEATURES

## source

Location/Qualifiers

1..744  
/organism="Poncirus trifoliata"  
/mol\_type="mRNA"  
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/clone="PT\_68A0011p17"  
/issue\_type="Phloem"  
/dev\_stage="10 - 30 cm shoots"  
/lab\_host="E. coli TUC121"  
/clone\_11b="Poncirus trifoliata CTv-challenged cDNA  
library - AG12"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid;  
Site 1: EcoRI; Site 2: XhoI; Plants were grown in the  
greenhouse at University of California, Riverside. The  
selection was an open-pollinated (very probably selfed)  
seedling of Poncirus trifoliata cv Pomeroy that was  
selected as homozygous for the CTv resistance gene. The  
rootstock was sweet orange infected with citrus tristeza  
virus (CTV) isolate T514 over 1 year before sampling (CTV  
infected sweet orange, but not genotypes carrying the CTv  
resistance gene). Shoots 10-30 cm long were harvested in  
October 2000, and the green phloem (bark) was removed and  
frozen quickly in dry ice. Total RNA was extracted using  
TRIzol reagent (Gibco). Poly(A) RNA was purified, a cDNA  
library was made, and 0.5 million primary lambda cDNA  
clones were in vivo excised to give a population of  
phagescript SK(-) phagemids. All steps to this point were  
performed in the ML Roose lab at the University of  
California, Riverside by X. Ye. Phagemids were plated,  
plasmid DNA purified, cDNA clones archived, and DNA  
sequences determined bi-directionally using an ABI3730 at  
the Arizona Genomics Institute, University of Arizona  
(Klm, Kudrna, Stum, Misoetski, Wings). Chromatogram files  
were downloaded to UC Riverside (Close), then processed at  
UC Riverside (Manamaker) using the HarvEST pipeline  
(http://harvest.ucr.edu) to remove vector and cloning  
oligo sequences and various contaminants, and to trim to a  
high quality region. Sequences that retained a phred 17  
region of at least 100 bases were deposited to GenBank."

## ORIGIN

Query Match 16.1%; Score 247.8; DB 7; Length 744;  
Best Local Similarity 65.8%; Pred. No. 1.3e-48;  
Matches 360; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

Qy 852 TTGCGCGTACACAGCTTAGGCGGACACTATCAGTCGTGAGCGGCTTCGACATAGTGAG 911  
Db 742 TTCAAGGCGCATATTTGGGTGGCGAGCTGTCAATTTTAAGCGCTTTGATTTGGCTGA 683  
Qy 912 AATCTCAGACCGGATCCGAGTCAGCGCGGTGCTTTCGGGTGCCCAAAAGTAGGCAAC 971  
Db 682 AATGGGTGACTGACATCCCTGTGGCGGCGTGTGTGCGGTGCCCAAGATTGGGAAAC 623  
Qy 972 AAAAATTCACCAACTCTTGTGACTGTGATCCCAAACTTAATGTCTTCATGTAAGAAAT 1011  
Db 622 AAAGCATTTTAAGAAAGATGAAGAGTACAGCAAGCTGAAGATTGCAAGTGAAGAAC 563  
Qy 1032 GTATCAGACCGATCCCTGTATCCGCTGAAGTCAAGGTTTACGTGAACATAGGATC 1091  
Db 562 ACATTTATCTCATAGCACTACCCGGGAGGTTGCTGGGTACGTTAAACGGGAGCT 503



directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize

REFERENCE  
AUTHORS  
1 (pages 1 to 697)  
Kozik, A., Michelmore, R. W., Knapp, S., Matvienko, M., Rieseberg, L.,  
Lin, H., van Damme, M., Lavelle, D., Chevallerier, P., Ziegler, J.

**TITLE** Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y. Lat, Z., Church, S., Jackson, L. and Bradford, K. Lettuce and Sunflower ESTs from the Compositea Genome Project <http://compgenome.ucdavis.edu/>

**JOURNAL** Unpublished (2002)

**COMMENT** Contact: Alexander Kozlik [R.W. Michelmore]

FEATURES	Location/Qualifiers
SOURCE	1. .697



Qy 435 LAPPEEDPTPEF 446  
Db 401 LAPVEEVEPPEF 412

## RESULT 2

T04551  
hypochemical protein F28J12.210 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004

C/Accession: T04551

R/Author: M. Hilbert, H. Braun, M. Holzer, E. Brandt, A. Duesterhoeft, A. Bancroft, submitted to the Protein Sequence Database, February 1998

A/Reference number: Z15377

A/Accession: T04551

A/Molecule type: DNA

A/Residues: 1-419 <BEV>

A/Cross-references: UNIPROT:O49523; UNIPARC:UPI000004897F; EMBL:AL021710

A/Experimental source: cultivar Columbia; BAC clone F28J12

C/Genetics:

A/Map position: 4

A/Introns: 83/3; 211/3; 288/2

A/Note: F28J12.210

Query Match 33.1% Score 789.5; DB 2; Length 419;

Best Local Similarity 37.8%; Pred. No. 2.8e-55; Matches 168; Conservative 77; Mismatches 137; Indels 63; Gaps 8;

Qy 17 WPELGSNAGALNPLNDELRELLRCGDFCQVYDTFTINDONSSYCGSSRYGKADLLH 76  
Db WRDLSGQNMKMGMLQPLDRLRYIIHYGEMAGAYDTFNTESQFAGASISKDPFA 82  
Qy 77 KT---AFPGADRFDVAVLYATKAVSVEAFLLKSREKMDRESNMGVYVNSDET 132  
Db 83 KVGLEIAHP--YTKYKVKFIYATSDIHVPESFLPFIISRGWSKESNMGVAVTDQG 140  
Qy 133 SRVAGREVVYVNRGTGDEWVDVGAQLESAPHLRTQTTHVEKVENEEKSIHSS 192  
Db 141 TALGRRRIIVVSKRSVQPLEWEDFERGLVNA----- 173  
Qy 193 WYDFGNIMLGASAKDKGSDDDDDPKVMQGMNTIYTSBDPKSPFTKLARTQLQTK 252  
Db 174 -----IKIFG-----BENDQVQHGGVSYLSMGDBRSPTTKTNARDQVLR 215  
Qy 253 LKQMTKTKYKDELSTFTFGHSLGATLSVVSAPDIYEN-----LTTEIPTAVVECP 304  
Db 216 VGRLEKTKYKDEBSITIGHSIGALATLSATDIVANGVNRKSRPDKSCPVTAFVFSF 275  
Qy 305 KVGKKFOOLFDSYVNLVLRNVIDLPLPVKLMGVNIGLEIDSRKSTFLKDSK 364  
Db 276 RVGDSDFKRLPSGLEDIRLRLNLPDIPIYP--IGSEVGDFPDIITRKSPYMKSPG 333  
Qy 365 NPSDMNLQAILHVVSGMHGV-KGE-FKVNKRSVYALVNSKCDPLKEBCLVPPAMVVQN 422  
Db 334 NLATHTCLEGLYHGAAGTGTAKDLPHLDVRAIGLVNKSVDGLKDCQWPGKKRVLYKN 393  
Qy 423 KGMVLNKDGEVNLAPPEEDPTPEF 447  
Db 394 KGMAQQDDGSGWELVDEIDNEDLD 418

## RESULT 3

C86198  
hypochemical protein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C/Accession: C86198

R/Author: A. Ecker, J.R. Palm, C.J. Federspiel, N.A. Kaul, S. White, O. Alonso, Chin, C.W., Chung, M.K., Conn, L., Conway, A.B., Conway, A.R., Creasy, T.H., Dewar, K., ansen, N.F., Hughes, B., Hutzar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maitl, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: P96552

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-423 <STO>

A/Cross-references: UNIPROT:Q9LNC2; UNIPARC:UPI00000481DD; GB:A8005172; NID:g8844130; PII C/Genetics:

A/Map position: 1

Query Match 32.3% Score 770.5; DB 2; Length 423;

Best Local Similarity 37.0%; Pred. No. 9.2e-54; Matches 163; Conservative 73; Mismatches 150; Indels 55; Gaps 6;

Qy 17 WPELGSNAGALNPLNDELRELLRCGDFCQVYDTFTINDONSSYCGSSRYGKADLLH 76  
Db 9 WKVLSGQNMKMGMLDPLDRLRYIIHYGEMAGAYDTFNTESQFAGASISKDPFA 68  
Qy 77 KTAFA-PEGADRFDVAVLYATKAVSVEAFLLKSREKMDRESNMGVYVNSDET 135  
Db 69 RTGFLKANPFRYKTKYIYATASIKLPISEIYKSLSKDASRVQTNMGYIAVATDQKAM 128  
Qy 136 AGREVVYVNRGTGDEWVDVGAQLESAPHLRTQTTHVEKVENEEKSIHSSWYD 195  
Db 129 LGRDVIYVNRGTGDEWVDVGAQLESAPHLRTQTTHVEKVENEEKSIHSSWYD 160  
Qy 196 CFNINLGASAKDKGSDDDDDPKVMQGMNTIYTSBDPKSPFTKLARTQLQTKQ 255  
Db 161 VFPT-----DPKONPRIISGGMILDIYASRSRSPYDTSAQEQVGLER 205  
Qy 256 LMTKYKQETSLTFTFGHSLGATLSVVSAPDIY-----ENLT-----TTEIPTAVVECP 306  
Db 206 LLELYKDEBSITFTFGHSLGATLSVVSAPDIY-----ENLT-----TTEIPTAVVECP 265  
Qy 307 GNKKFQOLFDSYVNLVLRNVIDLPLPVKLMGVNIGLEIDSRKSTFLKDSKNP 366  
Db 266 GDNHFNKNVDSLOPLNLRNVDPVAPHPFLI--YSEIGVELEITLNTSTYKRLNF 323  
Qy 367 SDMNILQAILHVVSGMHGVKEFKVNKRSVYALVNSKCDPLKEBCLVPPAMVVQN 426  
Db 324 RNYNLTLEIYHGMAGMDDTGQVFLKEIGRDISLVNKGDLAKDEYLVSTPRTCLANKGML 383  
Qy 427 LNKDGEVNLAPPEEDPTPEF 447  
Db 384 QMDGTWKLTVHRDHDVD 404

## RESULT 4

P96552  
hypochemical protein F5D21.19 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C/Accession: P96552

R/Author: A. Ecker, J.R. Palm, C.J. Federspiel, N.A. Kaul, S. White, O. Alonso, Chin, C.W., Chung, M.K., Conn, L., Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maitl, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: P96552

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-527 <STO>

A/Cross-references: UNIPROT:Q9CBJ6; UNIPARC:UPI000009534; GB:A8005173; NID:g10092365; P

C:Genetics:  
A:Gene: FSD21.19  
A:Map position: 1

Query Match 29.5%; Score 703.5; DB 2; Length 527;  
Best Local Similarity 35.5%; Pred. No. 2.9e-48;  
Matches 169; Conservative 69; Mismatches 133; Indels 103; Gaps 14;

QY 17 WPELGSNMAAGLNLPLNDELRELLRCGDFCQVYDTFTINDONSVCSSRYGKADL-- 74  
DB 91 WREVGCGNMEGQJDDPNMNLRRRIIRGEPAQCYDSFDFPSPKTCGSCCKPSPDFL 150  
QY 75 -----LHKTAFPGGADRFVAVLYATAKVSVPFAFLKSRREKMDRESNMIGYVVSN 129  
DB 151 NLDLHLK-----GYTTRVYATSNINLPN-FFQKSLSSINQHANMGFAVAT 201  
QY 130 D--ETSRVAGREYVYVWRCGRDYEWVDVLAQLESANPLLTQOTTHEKVENEEKS 187  
DB 202 DEEVSRL-GRDVIAMRGVTYLEW1----- 228  
QY 188 IHKSMWDCRNINLGSASDKGSGDDDDDDPKVMQGMWTITSEDPKSPFTKLSART 247  
DB 229 -----YDL-----KDIICSANFGDDPSIKIEGFHDLTYKKEDSCKFSFARB 272  
QY 248 QLOTKLKQMTKKYKD-----TLSTTFAGHSIGATLSVSAFDIYE--NL-----TTEIPV 296  
DB 273 QVLAERVRLIEYGTSEEGHKTSTTVGHSIGASLALVSAYDIELNLNHNVPENNYKIP1 332  
QY 297 TAVVFGCPKYGNKKFQQLFDSYPMNLVHVNVIDLIPLYPVKL----- 340  
DB 333 TVFSFSGPRVGNLAFKRCDEL-GVKVLRYVNVHDKVPVSGIPTNEKQFOKYYEEKTS 391  
QY 341 --MOTVNIIGLEIDSKSTFLKDSKSPSDMHNLA1LHVSGMHWKYGK-----FKVYVK 394  
DB 392 FPMYSAAHVGVELADHKKSPLKPKTKDLCGCHNLEALHLVDYGHGDDEAEKRFCLVTX 451  
QY 395 RSVALVWKSDFLKEECIVPPAMVWVONKGMVNLKDGEMV--APPEDPPE 445  
DB 452 RDLALVWKSDFLKEGTHVPPCMKDEKGMVKNKGDMVLPDRPLEPHGPE 504

## RESULT 5

G84709  
probable 11pase [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: G84709  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Unayam, L.; Tallon, L.;  
eues, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: G84709  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-447 <STO>  
A:Cross-references: UNIPROT:O04340; UNIPARC:UPI00000485C5; GB:AE002093; NID:G1946364; P1  
A:Genetics:  
A:Gene: At2G30550  
A:Map position: 2

Query Match 28.8%; Score 686.5; DB 2; Length 447;  
Best Local Similarity 35.6%; Pred. No. 5.2e-47;  
Matches 160; Conservative 78; Mismatches 133; Indels 79; Gaps 14;

QY 16 TWPELGSNMAAGLNLPLNDELRELLRCGDFCQVYDTFTINDONSVCSSRYGKADL 75  
DB 22 TWRIQIGEDWDAGLMDMDPLRSELIRYGEWAQACDAFDPSPAKTCGTSRTRHLEFF 81  
QY 76 HKTAFPGGADR-FPVVAVLYATAKVSVEAFLLKSRREKMDRESNMIGYVVSNDTSR 134  
DB 82 DSL-----GMIDSGEVARLYATSNINLPN-FFSKSRMSKWSKANMMGYAVVADDETSR 137

QY 135 -VAGREYVWRCGRDYEWVDVLAQLESANPLLTQOTTHEKVENEEKSIHKSWS 193  
DB 138 NRGDRDIALAMGTATYKLEMIADLKDYLPV-----TENNR----- 175  
QY 194 YDFENINLGSASDKGSGDDDDDDPKVMQGMWTITSEDPKSPFTKLSARTQOTKL 253  
DB 176 --C-----PDPVAVKESGFLDLYTDKDTCKPAPFSAREQILTEV 213

QY 254 KQMTKKYKD-----TLSTTFAGHSIGATLSVSAFDIYE--NLTE--LPYAVVGC 304  
DB 214 KLYVEHGDGDDDLSTTVGHSIGALALISAYDLAEMRLNBSKKGKVIPTVLYTGGP 273  
QY 305 KVGKFKQOLFDSYPMNLVHVNVIDLIPLYPVKLWG-----YVNI 347  
DB 274 RVGNVRFREMBEL-GVKVRVNVHVDVPSKGLPLNBSRPHAMKLAGLPMCYSHVG 332  
QY 348 IELEIDSRKSTFLKDSKNPSDMHNLA1LHVSGMHWKYGK-FKVNKRSVALVWKSDF 406  
DB 333 EELALDHQNSPFLKPSVDVSTAHNLBAMHLHDGYHG-KGBRFVLSGRDHALVWKSDF 391  
QY 407 LKEECIVPPAMVWVONKGMVNLKDGEMVLA 436  
DB 392 LKEHLQIPPEWRODANKGMVNRNSEGRWIOA 421

## RESULT 6

H86202  
hypothetical protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: H86202  
R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chun, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creeasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Hutzler, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Malt, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, L.  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: H86202  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-515 <STO>  
A:Cross-references: UNIPROT:Q9W9Y7; UNIPARC:UPI00000481E6; GB:AE005172; NID:G7523699; P1  
A:Genetics:  
A:Map position: 1

Query Match 28.1%; Score 670; DB 2; Length 515;  
Best Local Similarity 35.1%; Pred. No. 1.3e-45;  
Matches 157; Conservative 73; Mismatches 141; Indels 76; Gaps 12;

QY 16 TWPELGSNMAAGLNLPLNDELRELLRCGDFCQVYDTFTINDONSVCSSRYGKADL 75  
DB 88 TWRIQIGEDWDAGLMDMDPLRSELIRYGEWAQACDAFDPFSRYCSCRTTRHLEF 147  
QY 76 HKTAFPGGADR-FPVVAVLYATAKVSVEAFLLKSRREKMDRESNMIGYVVSND-ETSR 134  
DB 148 DSLGIDSG--YEVARLYATSNINLPN-FFSKSRMSKWSKANMMGYAVVSDNATR 204  
QY 135 V-AGREYVWRCGRDYEWVDVLAQLESANPLLTQOTTHEKVENEEKSIHKSWS 193  
DB 205 CRLGRDIALAMGTATYKLEMIADLKDFLPV-----SGNG 240  
QY 194 YDFENINLGSASDKGSGDDDDDDPKVMQGMWTITSEDPKSPFTKLSARTQOTKL 253  
DB 241 FRC-----PDPVAVKESGFLDLYTDKDTSCNFSKFSAREQILTEV 280  
QY 254 KQMTKKYKD-----TLSTTFAGHSIGATLSVSAFDIYE--NLTE--LPYAVVGC 304

Db 281 KRLVRYGDEBGEELSTVTGSHSLGALAVLSAYDVAMGVNRTRKGVIPVTAFTVCGP 340  
Qy 305 KVGKKKPPQQLFDSYPNLVNVLHVRNVIDLPLYP-----VKLMG-----YVNI 347  
Db 341 RVGIRFERERLEKT-GVAVLVVVEHDVAVKSPGLFLNERPQALMKLAGLPMCYSHVG 399  
Qy 348 IELIDSRKSTFLKDSKNPSDMNLQALILHVSGMGVKGFEKVVNKRKSVLVNKSDFL 407  
Db 400 EMLDLHDHQSFPKLPFTVDLSTRAHNLDAHLHLLDDGTHGKGQKFPVLSGRDPALVVKASDFL 459  
Qy 408 KEKCLVPPAMVNVONKGMVNLKDGWV 434  
Db 460 KDHFVPPVYVRQDANKGVNRYTDRWMI 486

## RESULT 7

Probable lipase [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: B44716  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanlaeken, S.E.; Umayam, L.; Tallon,  
L.; Euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
J. Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617157  
A:Accession: B84716  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Reads: 1-355 <STO>  
A:Cross-references: UNIPROT:O82274; UNIPARC:UPI0000485CD; GB:AE002093; NID:g3746065; P1  
A:Gene: At2g31100  
A:Map position: 2

Query Match 25.8%; Score 616; DB 2; Length 355;  
Best Local Similarity 32.9%; Pred. No. 1.6e-41;  
Matches 146; Conservative 69; Mismatches 111; Indels 118; Gaps 8;

Qy 17 WPELGSNAGLPLNDELRELLRCGDFCQVYTFINDONSYYGSSRYGADLLH 76  
Db 9 WKELSGSKMDLPLDLRLRYILHYGDMAEII-----AATPKKSSLL 54  
Qy 77 KTAFFGADRFDVAVYLATAKVSVPFAFLKSRREKMDRESNMGVAVVNDSTSYA 136  
Db 55 P-----VTSKPTL-----SDEGKLL 70  
Qy 137 GRREYVVMRGTCRDYEWVDVLGAQLSAPLLRTQOTTHVEKVENEEKSIHKSWDY 196  
Db 71 GRRGIVAMRGITQIYEMANDDPPLPSA----- 99  
Qy 197 FNINILSGASDKGKSGDDDDDDPKVMGMMTIYTSDEPKSPFYKLSARLOLTKLQ 256  
Db 100 --VWVFPGA-----NPDEBRVANGMSTLYSTDPSPRPKTSAOEQVDELR 147  
Qy 257 MTKYDEFLSTFAGSISGATLSVVSAPDIVN-----LTIDIPYAVFEGCPYGN 308  
Db 148 LELYNNEVVTITLTHSISGAVMSILSADFLHNPKTTPSLQHSLLCTVPAFGSPQIG 207  
Qy 309 KKFQOLFDSYPNLVNVLHVRNVIDLPLYPVKLMGVNIGIELEIDSRKSTFLKDSKN 368  
Db 208 RSPFKLVSLHHTLIRATNVDPDLIRYPV--FRFTDGEELQINTLKSSEVYKRLNIGH 265  
Qy 369 WHNLOALILHVSGMGVKGFEKVVNKRKSVLVNKSDFLKEKCLVPPAMVNVONKGM 428  
Db 266 FHNLEAYLHGVAGTQHNOGEFLTEINRDIATLVNKGILDLELDKYLVPGHVWVLENKGM 325  
Qy 429 KDGWV-----APREDPTP 445  
Db 326 DDGTWKLNGDSRKKQDEDEKEE 349

## RESULT 8

Probable lipase [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: A86428  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federle, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Hultzer, L. Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltli, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I.  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: A86428  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Reads: 1-529 <STO>  
A:Cross-references: UNIPROT:Q9C8G6; UNIPARC:UPI0000482FD; GB:AE005172; NID:g11055819; P1  
A:Gene:  
A:Map position: 1

Query Match 25.4%; Score 606.5; DB 2; Length 529;  
Best Local Similarity 32.0%; Pred. No. 1.7e-40;  
Matches 151; Conservative 79; Mismatches 157; Indels 85; Gaps 15;

Qy 1 MAAEQPLGSKPGPTPELIGSNAGLPLNDELRELLRCGDFCQVYTFINDON 60  
Db 104 MTPAAS--BEKISKMRRELGSNMWNELDLPHWRREYTKXGEFVESYSLDDPL 161  
Qy 61 SSYCGSSRYGADLLHKTAPFGADR--FDVAVLVATAKVSVEAFLLKSRSEKMDRE 118  
Db 162 SEFCSSRYNKNKLFEEL---GLTRGIVYTKIYMSKVDVDFWF--LSALGETSKD 216  
Qy 119 SNMIGYVNSDERTSVAGRREYVVMRGTCRDYEWVDVLGAQLSAPLLRTQOTTHVE 178  
Db 217 SNMIGFVAVSGDRSLNIGRDIYVAMRGYTPFEWMDLRTSMEP----- 262  
Qy 179 KVNEEEKSIHKSWSYCCFNINILSGASDKGKSGDDDDDDPKVMGMMTIYTSDEPKS 238  
Db 263 -----FDC-----EGK---HGKTVVYQSGFSLYNSKSELT 291  
Qy 239 PFTLSARLOLTKLQMLTKYD--EPLSTFAGSISGATLSVVSAPDIVNLTTEIP- 295  
Db 292 RYNRESASBQTMDEVKLVNFEFKDGEVSLITGHSLGALAMAYEAR---DVFA 347  
Qy 296 ---VTAVVFGCPKVGKKFQQLFDSYPNLVNVLHVRNVIDLPLYP-----VKLMG----- 342  
Db 348 LSGNISVIFGAPRVGNLAFREKLNLSL-GVAVLVVVKODIVPFLPGVFNKVLNKLNPI 406  
Qy 343 -----YVNIIGIELEIDSRKSTFLKDSKNPSDMNLQALILHVSGMGVKGFEKVVNKR 395  
Db 407 TSLRNWYVRHVGTLQKLDVFSPPYKRDSDIGRAHNLEVYLHVLVDGFRKKSGFRVAVAR 466  
Qy 396 SVALVNSCDFLKEKCLVPPAMVNVONKGMVNLND-GEWV--LAPREDPTP 444  
Db 467 DVASVNSKTDMLDLHLRIPEFWGVANHGLTNKQIGRWAKVPAAPEDIPSP 518

## RESULT 9

Probable triacylglycerol lipase - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
A:Variety: Columbia  
C:Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 09-Jul-2004  
C:Accession: E71435  
R:Bevan, M.; Bancroft, I.; Bent, B.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk  
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terry, N.; Giel  
avanagh, T.; Hempel, S.; Kotter, P.; Emtian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.  
Nature 391, 485-488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pigdomenech,  
erholt, A.; Mooren, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; And  
C.: Chalwatzi, N.  
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thaliana  
A:Reference number: AT1400; MUID:98121113; PMID:9461215  
A:Accession: E71435  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-601 <BEV>  
A:Cross-references: UNIPROT:O23522; UNIPARC:UPI0000048970; GB:I29734Z; NID:g2245031; PID:  
C:Genetics:  
/:Map position: 4COP9-4G3845

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Query March 18.6%; Score 442.5; DB 2; Length 601;
Best Local Similarity 30.0%; Pred. No. 2,66-27;
Matches 128; Conservative 60; Mismatches 126; Indels 113; Gaps 14;

QY      11 SKPEPTPELIGSNAMAGLNPINLDELRELLRCGDFCQCYDTTFINDQNSYCGSSRYG 70
Db      125 SKLGSKRRELGLNNMAGLDPIDLENLRRELYVRGEFVOAAYHAHFSHPDPE---GSPRH- 179

QY      71 KADLLHTAPFGAGDRPDVVAUYATATAKVSYPEAFLKRSREKXK-----PRES 119
Db      180 -----VALPDGS--FRVTKSLYATSSVRLP-----KRIIDVAPDLKRMTKQT 219

QY      120 NWIGYVAVSNDETS--RVAAGREVVYVMGTCRDYEWVDVIGAOLSAHPILRTQOTTHE 178
Db      220 SWAGYVAVVACDDPREIRRMGRREIVIALRGITLLEW----- 255

QY      179 KVENBEKKS IHKSSWYDCFNINILGASAKDQKGSDDDDDDPKYMGOMMTYTSSEPKS 238
Db      256 -SEN-----FRPNLV-SMEPEK---PDQSDPRPRKVECGFNSLYTTGQHA 296

QY      239 PFTYLSARTQLQTLKQLMTKYKDETLSTIFAGHSLGATLSVSAFDIVENTLTELIVTA 298
Db      297 P-----SLAESLIVGEISRLVELYAGEEELISVYTGSHISGAIALLAADDIAERVPAPAV 352

QY      299 VVEGCPKVGKKPQQLPDSYPNLVLVLRNVIIDILPLYP----- 337
Db      353 FSGFGPRVGNKEFPDRDLS--KGVKYLVRVNSQDVVTKVPGIFADNDKOGOSRRNKGSPGG 411

QY      338 -VKLM-----GYVNIIGIELEIDSRKSTFLKDSKNPSPDMNLQAILHVSGMHWKGEFK 390
Db      412 IMEYVERNNPWAYSHVGAEFLRVDKMGSPYLFKPNADVACCHDLKAYLHLVDGFLASNCPR 471

QY      391 VVNRKSV 397
Db      472 ANAKRSL 478

```

RESULT 10  
H84723  
Probable triacylglycerol lipase [imported] - *Arabidopsis thaliana*  
C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: H84723  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Unayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
/Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: H84723  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-484 <STD>  
 A:Cross-references: UNIPROT:Q9SIN9; UNIPARC:UPI00000485D3; GB:AE002093; NID:g4582461; PIR:PIR00000485D3  
 C:Genetics:  
 A:Gene: ATG31690  
 A:Map position: 2  
 Query Match 18.2%; Score 435; DB 2; Length 484;  
 Beet Local Similarity 27.8%; Pred. No. 7.7e-27;

	Matches	126;	Conservative	74;	Mismatches	134;	Indels	120;	Gaps	14;
Oy	7	PLGSKRPP-----TWPELLGSNMAGLNPINDLRRELLCGD	46							
Db	62	PVASSPPIIYCAPKPCSSGAATVPPLSRVMEHIQCCNNMKDLIEPLNPLLQOEITRYGN	121							
Oy	47	FCQVYDFPFINDONSSYCGRSRRYGADLIHKTAPFGADRFDVAAVLATATAKVSVEPAFL	106							
Db	122	LVTCTCYKAFDDPNKRILYNCKKYKGQTLLKEFIIDQPED-YQYTKXIYAT----PDINI	175							
Oy	107	LKSRSRKWDRESNMIGYYVSVNDERTRVAGRREVIVVMRGTRDVENVDVLGAQLESA-	165							
Db	176	NISPLQNEMNRRAARVGVVAASDDSVKRLGRDIYVTRGTVTNPWMLNFMSLSLPAR	235							
Oy	166	-HPLLRTQOTTHEKVENEEKSIHKSSWYDCFINILGSASKDKSGSDDDDDDEPKVM	224							
Db	236	FHP-----HNPL-----DYKVE	248							
Oy	225	QGMMTIYSEDPSFPFKLSARTLOTLKULKOIMTKKYDELSTTFPGHSLGATISVVSAP	284							
Db	249	SGFSLSYTSDSEBSFEGLESRCQOOLSEISRLMNKXKGEEMSTTLGHSHSGSSLAQLLA	308							
Oy	285	DIVE-NLT-----IPVTAVVFGCPKVGKKFOOLFDSYPNLNVLVRVAVIDLIPLYP-	337							
Db	309	DIABGLARRICKGDIPYTVFSFAGRGVGNLFERKGCBEI-GVKVLRITVNNDPVYTLPG	367							
Oy	338	-----VTLMG-----YNIIGILEIDSRSKSTFLKOSKNPSDMWNLOAILHAVS	380							
Db	368	VLFENEPFVLGGFYELPWSCSCYHVHGVELTLTD-----FFDVONISCVADLQTYIDLLN	421							
Oy	381	GMHGVKGFEEKVYNNKRSV-----ALVNYKSCDFLK	408							
Db	422	Q-----RRTNSKSVSDSDDEDSDNVALFEFLK	447							

RESULT 11  
 E86192  
 hypothetical protein [imported] - Arabidopsis thaliana  
 C|Species: Arabidopsis thaliana (mouse-ear cress)  
 C|Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #ext\_change 09-Jul-2004  
 C|Accession: E86192  
 R|Theologidis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 Hansen, N.F.; Hughes, B.; Huizart, L.  
 Nature 408, 815-820, 2000  
 A|Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.,  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitli, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A|Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.  
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A|Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A|Reference number: A86141; MUID:21016719; PMID:11130712  
 A|Accession: E86192  
 A|Status: Preliminary  
 A|Molecule type: DNA  
 A|Residues: 1-471 <STO>  
 A|Cross-references: UNIPROT:Q9M446; UNIPARC:UPI00000A8FAC; GB:AE005172; NID:g66850308; PIR  
 C|Genetics:  
 I|Map position: 1

Query Match	17.3%	Score 412.5	DB 2	Length 471
Best Local Similarity	28.4%	Pred. No. 4.7e-25		
Matches	123	Conservative	72	Mismatches 139, Indels 99, Gaps 11

  

QY	3	A	E	A	P	L	G	S	K	P	E	P	T	P	E	L	G	S	N	A	M	A	G	L	N	P	L	N	D	E	L	R	E	L	R	C	G	D	F	C	V	T	D	T	P	I	N	D	O	N	S	62		
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
Db	73	A	P	A	V	L	P	L	P	S	R	---	V	K	R	E	I	O	G	S	N	M	E	N	T	I	E	P	L	E	P	L	O	E	I	T	R	Y	N	L	S	A	S	K	G	D	L	N	S	K	129			
QY	63	Y	C	G	S	R	Y	K	A	D	L	L	H	K	T	A	F	P	G	A	R	P	D	V	A	Y	A	T	A	K	A	S	V	E	A	E	L	L	R	S	R	S	E	K	D	R	E	S	N	W	I	122		
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
Db	130	R	Y	L	S	C	K	Y	K	O	N	L	L	K	S	G	I	-	H	D	P	G	Y	Q	V	T	K	I	A	T	P	D	I	N	L	N	P	I	K	N	E	P	R	A	R	-----	W	I	180					
QY	123	G	Y	V	V	S	N	D	E	T	S	R	V	A	G	R	E	V	Y	V	V	R	G	T	C	R	D	Y	E	N	V	I	G	A	O	L	S	A	H	P	L	L	R	T	O	O	T	H	E	K	E	N	182	

```
Db 181 GYVAVSSDESIVKRLGRDILVTFRGVTYNHEWMLANLKSLTPA----- 223
Qy 183 BEKSIKSSWYDCFNINILGASAKDKGSGDDDDDDPKVMQGMNTIYTSDEKSPPTK 242
Db 224 -----RLDPNRPDPVKVSGSFLGLYTSSESSEKFG 255
Qy 243 LSARTOLTKLKQMTKYKDETLSTTFAGHSLGATLSVSAFDIVE---NLTFE---IPV 296
Db 256 ESCEQLLSERSLMKNHKGSEISITLAGHSMSSSLAGLADYDAELGMQRDRKPVV 315
Qy 297 TAVFSGCPKVGKPKFQOLFDSYPMNLVLRNVNIDLPYVVKMG----- 342
Db 316 TVFSPAGPRVGNLGFKKRCEEL-GVKVLRITNVNDPIKFLPGFLFENFRSLGGVYELPW 374
Qy 343 ----YVNIETLEIDRSKSTFLKSKSPSDMHNLOALIHVSGMHGK------GEF 389
Db 375 SCSCYTHVGVELTD-----FPVQNTSCVHDETYITTLVNRPRCSKLAVNEDNFGGEF 428
Qy 390 KVNKRSAVALVVK 402
Db 429 --LNRKSELMSFK 439
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## RESULT 12

T01607

probable triacylglycerol lipase AC2g44810 [Imported] - Arabidopsis thaliana

N;Alternate names: hypothetical protein F16B22.30; hypothetical protein T13E15.18

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 19-Feb-1999 #sequence revision 19-Feb-1999 #text\_change 09-Jul-2004

C;Accession: T00412; T01607; A84883

R;Rounsailey, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masc

submitted to the EMBL Data Library, July 1997

A;Description: Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence.

A;Reference number: Z14146

A;Accession: T00412

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-357 &lt;ROW&gt;

A;Cross-references: UNIPROT:O22170; UNIPARC:UPI0000048665; EMBL:AC002388; NID:g3420042;

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsailey, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Wolfat, K.S.; Cronin, L.A.; Shen, M.; Yanknen, S.E.; Unayam, L.; Tallon, L.

euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: A84883

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-357 &lt;STD&gt;

A;Cross-references: UNIPARC:UPI0000048665; GB:AE002093; NID:g344903; PIDN:AC31843.1; G

C;Genetics:

A;Gene: At2g44810, T13E15.18, F16B22.30

A;Map position: 2

Query Match 16.9%; Score 404; DB 2; Length 357;

Best Local Similarity 29.6%; Pred. No. 1.5e-24;

Matches 124; Conservative 60; Mismatches 131; Indels 104; Gaps 15;

```
Qy 79 AFGGADRFDVAVLYATAKVSPPEAFLLKRSREKM-DRESNWIGVYVNSD--ETSRV 135
Db 62 GLRNSGYR--LTNLRATSGINLPR-WIEKAPG---WMAQSSWIGVAVACODEEISRL 115
Qy 136 AGREVVYVVRGCRDYEWVDVLAQLESAPHLRTOQTHVEKVENBEKKSIIKSSWYD 195
Db 116 -GRDVVISFRGATCLEMLENLRATL-----THLPNGPT----- 149
Qy 196 CFNINILGASAKDKGSGDDDDDDPKVMQGMNTIYTSDEKSPPTKLSARTOLTKLKQ 255
Db 150 -GANLNGSN-----GPMVESGFSLYTS-----GVHSLRDVNRREIAR 187
Qy 256 LMTKYKDETLSTTFAGHSLGATLSVSAFDIVENLTFEIPVAVFSGCPKVGKPKFQOLF 315
Db 188 LIGSGDEPLSVTITGHSIGAAIATLAAVDIKTFKRAPMVTYVTSFGSPRGNRCFRKL 247
Qy 316 DSYPMNLVLRNVNIDLPYV-----VKMG-----YVNI 347
Db 248 EK-QGTQVLRIVNSDDVITVYVGVLENREODVYKMTASIMPSNIOREVEETPMVYAEIG 306
Qy 348 IELEIDRSKSTFLKSKSPSDMHNLOALIHVSGMHGKGFVKNRVALVVKSGDF 406
Db 307 KEKLRSRSDSPHL-SSINVAATCHELKTYLHLVDGF-----VSTCPF 347
```

## RESULT 13

S76637

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C;Accession: S76637

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yaeuda

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

sp.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S76637

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-407 &lt;KAN&gt;

A;Cross-references: UNIPROT:Q55826; UNIPARC:UPI00000C0F74; EMBL:D64004; GB:AB001339; NID

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 6.8%; Score 162.5; DB 2; Length 407;

Best Local Similarity 20.7%; Pred. No. 3.8e-05;

Matches 82; Conservative 59; Mismatches 127; Indels 129; Gaps 15;

Qy 19 ELGGSNMAWGLINPLNDELRELLRCGDFCOVYTFINDONSYYCGSSRYGKADLLHKT 78

Db 90 EINSVALTPILPYPYDQISQLLRCKINQOYL--GKTIPEYDGNIR-----QLP 140

Qy 79 AFGGADRFDV-----ALVYATKVSPEAFLLKRS---REKMDRESNMIGYVVS 128

Db 141 AYSDLDLVYQIASFRGRAHISSEVAQIP-----LNTGDPDLKTDQADEDSIG----- 191

Qy 129 NDERS-----VAGREVVYVVRGCRDYEWVDVLAQLESAPHLRTO 172

Db 192 --ETIRVVVKVTOGIPYVYLGITSSPRNLIIVFGTGTMEWVA-----NLBAQ 238

Qy 173 QTHVEKVENBEKKSIIKSSWYDCFNINILGASAKDKGSGDDDDDDPKVMQGMNTIYT 232

Db 239 QIPTEKRSQYFGKIH-----QGFIEHY- 262

Qy 233 SEDKSPPTKLSARTOLTKLKQMTKYKDETLSTTFAGHSLGATLSVSAFDI---VEN 289

Db 263 -----LRIVSPIPREIAOOLDPVAVCYVTGHSIGASLAVLALDVAVLNPN 308

Qy 290 LTFEIPVAVFSGCPKVGKPKFQOLFDSYPMNLVLRNVNIDLPYV--VKMGVYVNI 347

Db 309 LRSQIDLYS--YACPRVGDVTFQAL-HSROVPNSYRIVNLADVILPLPTTGGLGTVAHV 365



QY 348 ILEIDSRKSTPLKDSKNPDMNLQAILHVSQMHG 384  
 DB 366 QSMSPFSGGSDILPN-----HVDITYQG 388

## RESULT 14

106657

hypothetical protein T6G15.100 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear crease)

C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004

C/Accession: T06657

R/Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, April 1999

A/Reference number: Z15791

A/Accession: T06657

A/Molecule type: DNA

A/Residues: 1-805 &lt;BEV&gt;

A/Cross-references: UNIPROT:Q9T0H5; UNIPARC:UP1000009C968; EMBL:AL049656; GSPDB:GN00062;

A/Experimental source: cultivar Columbia; BAC clone T6G15

C/Genetics:

A/Gene: ATSP:T6G15.100

A/Map position: 4

A/Intons: 89/3; 112/2; 135/3; 163/1; 193/3; 539/3; 560/3; 587/2; 625/2; 652/3; 690/3; 7

Query Match 5.5%; Score 131.5; DB 2; Length 805;

Best Local Similarity 22.2%; Pred. No. 0.03; Mismatches 101; Indels 105; Gaps 13;

Matches 73; Conservative 50; Mismatches 101; Indels 105; Gaps 13;

QY 96 TAKVPEAPFLKSRKEMDRSNMIGYVVSNDSTRVAGREVVYVWRGTCRDYEW 155

DB 378 TAAAGTESGLATADTREADDEKED--GQVAINASKSLADMKNAQELAK-----QAD 429

QY 156 DIVLGA--QLESAPLRLTQOTTHVEKVENEEKSIHK---SSWYDCFNILGASADKG 210

DB 430 NVGALMLVLRKAVP-----HLKSDVSGSEKVIENKSSVVD---DVSGSKTEKI 477

QY 211 KSGDDDDDDPKVMQGMNTIYTSDEP-----KSPFTKL----- 243

DB 478 SGLVNDGADKBAEKMTLFSHSAESAMAMLATLGHPSFKSEFEKCLPLENDITD 537

QY 244 -----SARTQLTKLKQLMTKYKDET-----L 265

DB 538 TVQAIWRDARKRKVIAFRCTEQVHSGFLSAYDSVRIRIISLKMITGIDYDTERDKW 597

QY 266 SITPAGHSGLATISVVSAPFIVENLTTE---IPTAVVFCGPKYGNKKFQOLF-----DS 317

DB 598 HVVVTGHSISGLALATLALSLSSQLAKGAIIVTMNFGSPRYGNKQFAIYVQKVKDS 657

QY 318 YPNLNVLHVRNVIDLPLYPVKLMGYVNI 346

DB 658 W-----RVNHRDILITVP-RLMGYCHV 679

## RESULT 15

S64146

probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein G2842

C/Species: Saccharomyces cerevisiae

C/Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 09-Jul-2004

C/Accession: S64146; S71739

R/Bacriano, V.; Eraso, P.; Portillo, F.; Mazon, M.J.

submitted to the Protein Sequence Database, May 1996

A/Reference number: S64144

A/Accession: S64146

A/Molecule type: DNA

A/Residues: 1-1264 &lt;ESC&gt;

A/Cross-references: UNIPROT:P51125; UNIPARC:UP10000052E2A; EMBL:Z72655; NTD:G1322701; PI

R/Bacriano, V.; Eraso, P.; Portillo, F.; Mazon, M.J.

Yeast 12, 887-892, 1996

A/Title: Sequence analysis of a 14.6 kb DNA fragment of Saccharomyces cerevisiae chromos

A/Reference number: S71733; MUID:96437978; PMID:8840506

A/Accession: S71739

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-1264 &lt;ESW&gt;

A/Cross-references: UNIPARC:UP10000052E2A; EMBL:X92670

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995

C/Genetics:

A/Gene: SGD:ITC1

A/Cross-references: SGD:S0003101

A/Map position: 7L

A/Keywords: transmembrane protein

F/549-565/Domain: transmembrane #status predicted &lt;TMM&gt;

Query Match 5.1%; Score 121; DB 2; Length 1264;

Best Local Similarity 20.7%; Pred. No. 0.4; Mismatches 135; Indels 82; Gaps 14;

Matches 72; Conservative 58; Mismatches 135; Indels 82; Gaps 14;

QY 153 EWDVILGAQLESAPLRLTQOTTHVEKVENEEKSIHKSSWYDCFNILGASADKG 207

DB 262 EWPXDMILKYEDEPPVARRNSANVSPSEKKNKQSKSG-----KSNTSNDASNKKETK 317

QY 208 DKGSGDDDDDDPKVMQGMNTIYTSDEPKSPFTKLARTQLTKLKQLMTKYKDET-L-S 266

DB 318 KKKKPTFVNDSEN-----NSSEEDKKKGQNTSETHSKRKKEANEPEPTVEVES 367

QY 267 ITPAGHSGLATISVVSAPFIVENLTTE---IPTAVVFCGPKYGNKKFQOLF-----DS 317

DB 368 VPTPANAEPQAVTITIMDLALPYQHPNIPNLITYNEKLCISGTYKLSRPFDSFG 427

QY 318 -----YPNLNVLHVRNVIDLPL-----YPVKLMG---YVNI-----GIELTISR 355

DB 428 KLIQAVQPLNTFSGSKCLSHFSIDQFTISLKTCDPFLKGEVVLVNIROTSGEQLENN 487

QY 356 -----KSTPLKDSKNPDMNLQAILHVSQMHGKGEFQV-----NK 394

DB 488 GLPMKKKAETTTEDSENPSDMQNSFIRDMIKRSDKVEYKIVHDDPASDDILDNINH 547

QY 395 RSVLVNKSCD-----FLKE-----CLVPPAMVNVQKKGVNLKQGE 432

DB 548 NSGALLIEVFTALLRLFINEGDMSCIVEN-WIIDKGVLMEKDE 593

Search completed: December 22, 2005, 19:47:51  
 Job time : 28.5 sec

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: December 22, 2005, 19:19:46 ; Search time 147.5 Seconds

(without alignments)  
2138.110 Million cell updates/sec

Title: US-10-674-540A-2  
Perfect score: 2385  
Sequence: 1 MAAEAPGLGSKPGPTWPEL.....NKDGWVLAPPEEDPTPEFD 447

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2385	100.0	447	2	092TW1_DIACA
2	1311.5	55.0	412	2	092TW1_ARATH
3	1057	44.3	465	2	092TW1_ARATH
4	789.5	33.1	419	2	092TW1_ARATH
5	770.5	32.3	423	2	092TW1_ARATH
6	767.5	32.2	423	2	092TW1_ARATH
7	755.5	31.7	411	2	092TW1_ARATH
8	740.5	31.0	407	2	092TW1_ARATH
9	736	30.9	420	2	092TW1_ARATH
10	730	30.6	418	2	092TW1_ARATH
11	703.5	29.5	527	2	092TW1_ARATH
12	686.5	28.8	529	2	092TW1_ARATH
13	670	28.1	535	2	092TW1_ARATH
14	616	25.8	355	2	092TW1_ARATH
15	606.5	25.4	529	2	092TW1_ARATH
16	591	24.8	478	2	092TW1_ARATH
17	565	23.7	478	2	092TW1_ARATH
18	536	22.5	444	2	092TW1_ARATH
19	462	19.4	544	2	092TW1_ARATH
20	462	19.4	544	2	092TW1_ARATH
21	442.5	18.6	601	2	092TW1_ARATH
22	441.5	18.5	534	2	092TW1_ARATH
23	441.5	18.5	534	2	092TW1_ARATH
24	435	18.2	484	2	092TW1_ARATH
25	425.5	17.8	447	2	092TW1_ARATH
26	412.5	17.3	471	2	092TW1_ARATH
27	405.5	17.0	200	2	092TW1_ARATH
28	404	16.9	357	2	092TW1_ARATH
29	403	16.9	538	2	092TW1_ARATH
30	400	16.8	446	2	092TW1_ARATH
31	384.5	16.1	460	2	092TW1_ARATH

32	373.5	15.7	457	2	053M17_ORYSA
33	372.5	15.6	435	2	0851D9_ORYSA
34	351	14.7	440	2	05N8V4_ORYSA
35	225.5	9.5	244	2	05JIG2_ORYSA
36	207	8.7	324	2	06H7K1_ORYSA
37	170	7.1	91	2	08GXS9_ORYSA
38	162.5	6.8	407	2	0558Z6_SYNY3
39	144.5	6.1	273	2	06XIV5_PHYC
40	144	6.0	287	2	08WY67_DICDI
41	141.5	5.9	469	2	093JZ5_ARATH
42	140.5	5.9	469	2	08HID5_ARATH
43	140.5	5.9	507	2	09LUD3_ARATH
44	140	5.9	278	2	054E06_DICDI
45	140	5.9	888	2	07XQ16_ORYSA

## ALIGNMENTS

## RESULT 1

ID	Q92TW1_DIACA	PRELIMINARY;	PRT;	447 AA.
AC	Q92TW1;			
DT	01-MAY-1999 (TREMBlrel. 10, Created)			
DT	01-MAY-1999 (TREMBlrel. 10, Last sequence update)			
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)			
DE	Lipase (fragment)			
OS	Dianthus caryophyllus (Carnation) (Clove pink)			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Caryophyllales; Caryophyllaceae; Dianthus.			
OX	NCBI_Taxid=3570;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Petal;			
RA	MEDLINE=20359773; PubMed=10890894; DOI=10.1073/pnas.140213697;			
RA	Hong Y., Wang T.W., Hudak K.A., Schade F., Froese C.D., Thompson J.E.;			
RT	"An ethylene-induced cDNA encoding a lipase expressed at the onset of			
RT	senescence."			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:8717-8722(2000).			
RR	EMBL; AF026480; AAD01804.1; -; mRNA.			
DR	GO; GO:0004806; F:triacylglycerol lipase activity; IEA.			
DR	GO; GO:0006629; P:lipid metabolism; IEA.			
DR	InterPro; IPR002921; Lipase_3.			
DR	Pfam; PF01764; Lipase_3; 1.			
FT	NON_TER			
FT	1			
FT	447			
FT	SEQUENCE 447 AA; 50276 MW; 960D46B03153AC26 CRC64;			

Query Match 100.0%; Score 2385; DB 2; Length 447;  
Best Local Similarity 100.0%; Pred. No. 2.1e-177; Indels 0; Gaps 0;  
Matches 447; Conservative 0; Mismatches 0;

QY	1	MAAEAPGLGSKPGPTWPELGSNAAGLNPINDELRELLRCGDFCOVYDFFINDON	60
DB	1	MAAEAPGLGSKPGPTWPELGSNAAGLNPINDELRELLRCGDFCOVYDFFINDON	60
QY	61	SSYSGSSRYGKADILHKTAFPGGADRFVVAAYATKAVSYPBAFLKSRREKWDREBN	120
DB	61	SSYSGSSRYGKADILHKTAFPGGADRFVVAAYATKAVSYPBAFLKSRREKWDREBN	120
QY	121	WIGVVVSNDETSTVAGRRREVYVWRCRDYEVNDVLGAOLBSAHPILRTQOTTHVEKV	180
DB	121	WIGVVVSNDETSTVAGRRREVYVWRCRDYEVNDVLGAOLBSAHPILRTQOTTHVEKV	180
QY	181	ENEKKSIIHKSQWDCFNINILGSASDKGSGSDDDDDDPKVMQGMWITTSDDPKSPF	240
DB	181	ENEKKSIIHKSQWDCFNINILGSASDKGSGSDDDDDDPKVMQGMWITTSDDPKSPF	240
QY	241	TKLSARFQLOTKLQMTKTKYDEFTLSTPAGHSIGATLSVVSADIVENLTTEIPVNAV	300
DB	241	TKLSARFQLOTKLQMTKTKYDEFTLSTPAGHSIGATLSVVSADIVENLTTEIPVNAV	300

Qy 301 FGCPKVGKKEFQQLFDSYPNINLVHVRNVIDLIPYVKMGVYNGIELEIDSRKSTFL 360  
 Db 301 FGCPKVGKKEFQQLFDSYPNINLVHVRNVIDLIPYVKMGVYNGIELEIDSRKSTFL 360  
 Qy 361 KDSKNPSPDMNLQAILHVSGMHGKGFVKVYKRSVALVNKSCDFLKECLVPPAMVWV 420  
 Db 361 KDSKNPSPDMNLQAILHVSGMHGKGFVKVYKRSVALVNKSCDFLKECLVPPAMVWV 420  
 Qy 421 ONKGMVINKDGEWVLAPEEDPTPEFD 447  
 Db 421 ONKGMVINKDGEWVLAPEEDPTPEFD 447

## RESULT 2

Q9SUT7 ARATH  
 ID Q9SUT7\_ARATH PRELIMINARY; PRT; 412 AA.  
 AC Q9SUT7;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
 DE Putative lipase.  
 GN Name=A2942690;  
 OS A-Abidopsis thaliana (house-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC Fossids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]

RA NUCLEOTIDE SEQUENCE.  
 RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,  
 RA Barnstead M.E., Mason T.M., Bowman C.L., Rouning C.M., Benito M.-I.,  
 RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,  
 RA Fraser C.M., Venter J.C.;  
 RA Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 RL [2]

RP NUCLEOTIDE SEQUENCE.  
 RA Town C.D., Kaul S.;  
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.  
 RN [3]

RP NUCLEOTIDE SEQUENCE.  
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,  
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,  
 RA Caninui P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
 RA Kamliya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,  
 RA Seki M., Shim P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,  
 RA Theologis A.;  
 RA Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.  
 RN [4]

RP NUCLEOTIDE SEQUENCE.  
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etyou P., Lee J.M.,  
 RA Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,  
 RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shim P.,  
 RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;  
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AC006931; AAD21737.1; -; Genomic DNA.  
 DR EMBL; AC007087; AAM5382.1; -; Genomic DNA.  
 DR EMBL; AY050998; AAK3675.1; -; mRNA.  
 DR EMBL; AY079356; AAL65087.1; -; mRNA.  
 DR PIR; A84857; A84857.  
 DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.  
 DR GO; GO:0006628; P:lipid metabolism; IEA.  
 DR InterPro; IPR002921; Lipase\_3.  
 DR InterPro; IPR008262; Lipase\_AS.  
 DR Pfam; PF01764; Lipase\_3; 1.  
 DR PROSITE; PS00120; Lipase\_SSR; UNKNOWN 1.  
 SQ SEQUENCE 412 AA; 46057 MW; 4923CC470B4BEEF9 CRC64;

Query Match 55.0%; Score 1311.5; DB 2; Length 412;  
 Best Local Similarity 56.0%; Pred. No. 1.1e-93;  
 Matches 242; Conservative 72; Mismatches 91; Indels 27; Gaps 4;  
 16 TWPELLGSNNAMGLNPLNDELRELLNCGDFCYTYDFINDQNSVCGSSRYKADLL 75

Db 7 SWEELGSKWMDITLDDLDOSLRELLRCGDFCCATYDAFVNDSRYCQASRYGKSPFF 66  
 Qy 76 HKTAFCGADRFVAVLYATVYAKVSPFAFLKSRSHREKMDRESNMIGYVVSNDSTSRV 135  
 Db 67 DKVMLEASD-YEVVNLVYATARSVLEGLLQSGSDMSDRBNMGYLAIVSDERSKA 125  
 Qy 136 AGREVVYVWVWGRGCRDYEWVVDGQLESAPHLIRTOQTHVEKENEKKSIIKSSWYD 195  
 Db 126 LGRREIVIALRGTSRNVEMVNLGAPRPSADPLHGP-----EODSGGVVECTTFD 177  
 Qy 196 CFNINLLGSASKDGKSDDDDDPRVMOGMMTIYSEDPKSFTLSARTLOQTLLKQ 255  
 Db 178 -----SDSEDEGCKVMGLWLTITSNHPSEKFTLSRSQLLAKIKE 220  
 Qy 256 LMTKYDETSLTPAGHSLGATLSVSAFIVER-LTTEIPVTVAVPGCPKVGKKEFQQL 314  
 Db 221 LLLKTKDEKPSIVLTGSLGATEAVLAVIDAENGSDDVPTVAIVGCGQVGNKERFDE 280  
 Qy 315 FDSYPNINLVHVRNVIDLIPYVKMGVYNGIELEIDSRKSTFLKDSKNPSPDMNLQ 374  
 Db 281 VMSHKNLKILHVRNTIDLLTRYPGGLGYVDIGINFVIDTRKSPFLSDSRNPGDMNLQ 340  
 Qy 375 ILHVSGMHGKGFVKVYKRSVALVNKSCDFLKECLVPPAMVWVONKGMVINKDGEWV 434  
 Db 341 MLHVAVAGMNGKGFVKVYKRSVALVNKSCDFLKECLVPPAMVWVONKGMVINKDGEWV 400  
 Qy 435 LAPPEEDPTPEF 446  
 Db 401 LAPPEEDPTPEF 412

## RESULT 3

OSNAT4 ORYZA  
 ID OSNAT4\_ORYZA PRELIMINARY; PRT; 465 AA.

DT 01-FEB-2005 (TREMBLrel. 29, Created)  
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)  
 DE Lipase-like  
 GN Name=P0456F08.24;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OC NCBI\_TaxID=39947;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
 RA Mu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,  
 RA Hosokawa S., Maunukawa M., Arikawa K., Chiden Y., Hayaishi M.,  
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,  
 RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,  
 RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,  
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
 RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
 RA Namiki N., Negishi M., Ohta I., Ono N., Saito S., Sakai K., Shibata M.,  
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K.,  
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,  
 RA Yano M., Jiang J., Gojobori T.;  
 RT "the genome sequence and structure of rice chromosome 1.";  
 RL Nature 420:312-316(2002).  
 DR EMBL; AP002901; BAB81525.1; -; Genomic DNA.  
 DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.  
 DR GO; GO:0006629; P:lipid metabolism; IEA.  
 DR InterPro; IPR002921; Lipase\_3.  
 DR Pfam; PF01764; Lipase\_3; 1\_3.  
 SQ SEQUENCE 465 AA; 50453 MW; 5167A02D019F0EB CRC64;

Query Match 44.3%; Score 1057; DB 2; Length 465;  
 Best Local Similarity 46.8%; Pred. No. 9.5e-74;

Matches 206; Conservative 73; Mismatches 109; Indels 52; Gaps 6;

QY 11 SRGPTWPELGGNAGLNPDLRELLRCGDFCQVTPFFINDONSSVCGSSRYG 70  
 DB 17 SRP---WPELLGSAHMDGLDPLDLTRRLILLCGLDLCQVTPYFSFNDSHSKYCGTCRFS 73  
 QY 71 KALLHKTAPPGADRFVAVLYATAKVSPFAFLKSRSEKWDRESNMIGYVVVNSD 130  
 DB 74 RSTLLDRTPFAAGD--LSVAAYLYATSDATAFESQSMYSMSREMSKESNMIGYVVNSD 132  
 QY 131 ETSRVAGREVVYVWRGTCRDYEWVDVLAQLESAPHLRTQOTTHVEKVENEEKSIHK 190  
 DB 133 AAAAAGGQRIYVYAMRGITISLEWVDYLPKDL-----VDHDD----- 169  
 QY 191 SSAYDCENINLLGSASDKKSGSDDDDDPKVMQGMNTIYTSDEPKSPFTKLARTQLO 250  
 DB 170 -----ILPEGHPRGRS-----RWKKGWVLYTSDEKSPSKSARQML 210  
 QY 251 TKLKQMTKYKDETLSTTFAGSHLGLATLSVVSAPFIYENLTTE-----IPVTAVVGCP 304  
 DB 211 AAVRELAVARYANSLGVCTGHSIGASLATLCAFDIYVNGSVKVGDAHLPVTAVVGSP 270  
 QY 305 KVGKKKFOQLFDSYPNLNLVAVRNVDLPLYPVKLMGYVNIIGIEIDRSKSTFLDKSK 364  
 DB 271 QIGNPFKQFEBQPNLRALHVRNMPDLPLYPGGLGYANVGKTLQVDSKSPYVRDT 330  
 QY 365 NPSDMHNLAIIHVSGMHGVGFKVKNRSVALVNSCDFLEKCLVPPAMVYVONKG 424  
 DB 331 SPEDYHNLQGIILTVAGMNGKDEFLKQVNRVALVNSGFLDKSNLVPESMWVERNKG 390  
 QY 425 MVLNKGDEWVLAPEDEPTP 444  
 DB 391 MVLGNGEMQLEGPARENLP 410

## RESULT 4

049523 ARATH  
 ID 049523\_ARATH PRELIMINARY; PRT; 419 AA.

AC 049523;  
 DT 01-JUN-1998 (TEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)  
 DT 01-FEB-2005 (TEMBLrel. 29, Last annotation update)  
 DE Lipase-like protein.  
 GN Name=F28J12.210; Synonyms=Atg18550.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC euroids II; Brassicales; Brassicaceae; Arabidops.  
 OC NCBI\_Taxid=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,  
 RA Bancroft I., Mewes H.W., Mayer K., Schueller C.,  
 RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,  
 RA Mewes H.W., Lemcke K., Mayer K.F.X.,  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RA EU Arabidopsis sequencing project;  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AL021710; CA16735.1; -; Genomic DNA.  
 DR EMBL; AL161548; CAB78857.1; -; Genomic DNA.  
 DR PIR; T04551; T04551.  
 DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.  
 DR GO; GO:0006629; P:lipid metabolism; IEA.  
 DR InterPro; IPR002921; Lipase\_3.

DR Pfam; PF01764; Lipase\_3; 1.  
 SQ SEQUENCE 419 AA; 47792 MW; 3B2B13089146482C CRC64;

Query Match 33.1%; Score 789.5; DB 2; Length 419;  
 Best Local Similarity 37.8%; Pred. No. 6.2e-53;  
 Matches 169; Conservative 77; Mismatches 137; Indels 63; Gaps 8;

QY 17 WPELLGSNAGLNPDLRELLRCGDFCQVTPFFINDONSSVCGSSRYGKADLLH 76  
 DB 23 WRDLSCGNHKKMLQPLDQLREYIIHYGMAAGVDTFINESQAGASISRKDFFA 82  
 QY 77 KT---AFPGADRFVAVLYATAKVSPFAFLKSRSEKWDRESNMIGYVVNSDET 132  
 DB 83 KVGLEIAHP--YTKYKTKFIYATSDIHVESFLPFSREKGSKESNMIGYVAVTDQG 140  
 QY 133 SRVAGREVVYVWRGTCRDYEWVDVLAQLESAPHLRTQOTTHVEKVENEEKSIHK 192  
 DB 141 TALLGRDIYVSRGSGVPLEWDEFEGLVNA----- 173  
 QY 193 WYDCFNINLLGSASDKKSGSDDDDDPKVMQGMNTIYTSDEPKSPFTKLARTQLO 252  
 DB 174 -----IKIFG-----BRNDQVQIHQGMISITMSQDEBSFTITNARDVLR 215  
 QY 253 LKQMTKYKDETLSTTFAGSHLGLATLSVVSAPFIYENLTTEIPVTAVVGCP 304  
 DB 216 VGRLEKYKDEVSITICGHSIGALATLSATDIVANGYRPKSRPDKCPVTAFAVFPASP 275  
 QY 305 KVGKKKFOQLFDSYPNLNLVAVRNVDLPLYPVKLMGYVNIIGIEIDRSKSTFLDKSK 364  
 DB 276 RVGDSDFRKLFGSLIEDIRVLRNLPDVPVIPP--IGYSEVDEDEFIDRKSFPYKSPG 333  
 QY 365 NPSDMHNLAIIHVSGMHGV-KGE-FKVVNKRVALVNSCDFLEKCLVPPAMVYVON 422  
 DB 334 NLATFHCLGYLGVAGTQGTNKADLFRLDVERAIGLVNSVDGLKDECVNPKRVLKN 393  
 QY 423 KGVNKGDEWVLAPEDEPTP 447  
 DB 394 KGVNAQDDGSMELVDHIDNEDLD 418

## RESULT 5

09LNC2 ARATH  
 ID 09LNC2\_ARATH PRELIMINARY; PRT; 423 AA.

AC 09LNC2;  
 DT 01-OCT-2000 (TEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
 DE P9P14.11 protein.  
 GN Name=P9P14.11;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC euroids II; Brassicales; Brassicaceae; Arabidops.  
 OC NCBI\_Taxid=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sakano H., Vaysberg M., Lee J.M., Lenz C., Liu S.X., Pham P.,  
 RA Toriumi M., Yu G., Chiu J., Choi E., Chung M., Gonzalez A.,  
 RA Howing B., Liu A., Altafi H., Brooks S., Buehler E., Chao O., Conn L.,  
 RA Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,  
 RA Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,  
 RA Ecker J.R., Federapfel N.A., Theologis A.,  
 RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AC025290; AAF80222.1; -; Genomic DNA.  
 DR PIR; C86198; C86198.  
 DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.  
 DR GO; GO:0006629; P:lipid metabolism; IEA.  
 DR InterPro; IPR002921; Lipase\_3.  
 DR InterPro; IPR008262; Lipase\_AS.  
 DR Pfam; PF01764; Lipase\_3; 1.  
 DR PROSITE; PS00120; LIPASE\_SER; UNKOWN 1.  
 SQ SEQUENCE 423 AA; 48122 MW; E410984DC9F6DC74 CRC64;

Best Local Similarity 36.7%, Pred. No. 3,3e-51, Matches 162; Conservative 73; Mismatches 151; Indels 55; Gaps 6

```
OY 17 WPELLGSNANAGLPLNDELRELLKCGDCQYTTDTFTINDQSSYGGSSRYGKADLLH 76
Db 9 WKVLSSGNKMKGLLDPLDPDLRRYIHHGEMSVGYDAFNWDRKSRVAGDCYSSKNRLPA 68
OY 77 KTAI-PCGADRFVDVAIVATYAKVSVEPAFLIKRSRREKMDRESNMWIGVAVVNSDTSRV 135
Db 69 RTGFLKANKPFRKYKTKIYATASIKLPISEYKSLSDKASHVQTNMGIYAVATDGKAM 128
OY 136 AGREVVYVVRKGTGRDYEWDVLGAQLESAPHLRTQOTTHEKVENEEKSIHKSWMYD 195
Db 129 LGRDIIYVANKGLTPQPYEMANDPFLPEPA-----IS 160
OY 196 CFNINLLGASAKDKGKSGSDDDDDPKPMQGMWMTIYTSDEPKSPPTKLSARTQLOTKLQ 255
Db 161 VFPT-----DPKNPNRSGSMGLIYTASDSRSPYDTTSAEQVGELKR 205
OY 256 LMTYKQDETSLITFAGHSLGATLSVSAFDV----ENLT-----TEIPAVAVGCPKV 306
Db 206 LLELYKBEISITTTGSHLGAWSVLSADLVYKKNININLQKKQVPIYFAFGSPRI 265
OY 307 GNKKFQOOLFDSYPMLNVAVNVAVIDLIPYEVKLMGYNIGIELEIDRSKSTFLDSKNP 366
Db 266 GDHNFKNVVDLSQGLNLTIRIYNVDPVAHYFL--VSEIGEVLEINTLNSYTLKSLNF 323
OY 367 SDWNLQAILHVSQMGHVGKEFPKVNKRSVALYNKSCDPLKEBLUPPAMVNVNKGWV 426
Db 324 RNYHNLEIYHGMAGMOPDQVFLKEIGRDISLVNKGIDALKEYLVPSTWRCLANKWL 383
OY 427 LNKDGEVNLAPPEDDPTPEFD 447
Db 384 QMDGTYWKLVDVRRDDDDVD 404

RESULT 7
OY 06F358_ORYSA PRELIMINARY; PRT; 411 AA.
AC 06F358;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE Putative lipase.
GN Name=O01268_B08.3; Synonyms=O01735_C10.21;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubharoidae; Oryzaceae; Oryza.
OC NCBI_TaxID=39947;
OK [1]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsiang Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Lwu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsiang Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Lwu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL "Oryza sativa BAC O01735_C10 genomic sequence."
RL Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC104284; AAU44110.1; -; Genomic DNA.
DR EMBL; AC098832; AAT69580.1; -; Genomic DNA.
DR EMBL; O6F358; -;
DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.
```

DR GO:0006629; P:lipid metabolism; IEA.  
 DR InterPro: IPR002921; Lipase\_3.  
 DR InterPro: IPR008262; Lipase\_AS.  
 DR Pfam: PF01764; Lipase\_3; 1.  
 DR PROSITE: PS00120; LIPASE\_SER; UNKNOWN 1.  
 SQ SEQUENCE 411 AA; 45608 MW; 780C7A575A41959C CRC64;

Query Match 31.7%; Score 755.5; DB 2; Length 411;  
 Best Local Similarity 37.4%; Pred. No. 2,7e-50;  
 Matches 164; Conservative 65; Mismatches 150; Indels 59; Gaps 5;

QY 17 WPELLGSNANAGLNPINDELRELLRCGDFCQVYTPFINDQSSYCGSSRYGKADLLH 76  
 DB 15 WREIHGSDWDGLDPDLDRRTVIRYGEWAQATYDAFNHEKLSPHAGLSRFAARRFFE 74  
 QY 77 KTAFFPGADRFDDVAVYLYATATKSVVPEAFLLKSRREKMDRESNIGYVAVSNDETS 136  
 DB 75 RAQLPGHSAAYRVARFYATSCVAVPEPLILRSRRCRESNIGYVAVATDEGKAL 134  
 QY 137 GREVVYVNRGTCDYEWVDVLAQLESAPHLRTQOTTHVEKENEKKS IHKSSWYDC 196  
 DB 135 GRDDIVAMGTQVQSLWMIDMPVMPKGLR----- 168  
 QY 197 FNINLGSASAKDKGSDDDDDPKVMQGMNTIYTSDEPKSPPTKLSARTOLQTKLKL 256  
 DB 169 -----DKASDAMVHRGWLMSYTSRDSSSHKXOSARDQVLSVAKL 209  
 QY 257 MTKYKDELTSTFAGSLGATLSVSAFDIYEN-----LTTELPTAVAVFGCPKV 306  
 DB 210 VSMYQDELSITVYGHSLGALATLNAFDIYENGYNAPRAAAAAGCPPTAFVAFASPRV 269  
 QY 307 GNKKFOOLFDSYP--NINVLVHRNVLDLPLVYKLMGVNIGLEIDSKSTFLDSK 364  
 DB 270 GSGGFKRRFGARGGLRLRVRNARVPRYP-PAPPYHGVGELIDTGESFYLRPG 328  
 QY 365 NPSDMNHLQALILHVSQGMHGVK-GEFKVVKRSVALVNSCDFLKECELVPPAMVVQK 423  
 DB 329 NELVNHLECYLHGVAAGGEGAFKLAVERDVALLANKSYGALRDHAVAPAGWIMDSNR 388  
 QY 424 GMYLNGEYVLAPEED 441  
 DB 389 GMYRGADRGWTLMDREED 406

## RESULT 8

Q6F357\_ORYSA PRELIMINARY; PRT; 407 AA.

AC Q6F357;  
 DT 25-OCT-2004 (Tremblrel. 28, Created)  
 DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
 DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)  
 DE Putative lipase.  
 GN Name=OJ1268\_B08.4; Synonym=OJ1735\_C10.22;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OC NCBI\_TaxID=39947;  
 RN NCBI\_TaxID=39947;  
 RP NUCLEOTIDE SEQUENCE.  
 RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,  
 RA Chen Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,  
 RA Hsiung U.-N., Hsu C.-H., Huang J.-J., Han S.-Y., Hsiao S.-H.,  
 RA Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,  
 RA Wu H.-P., Shaw J.-F.;  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

RP NUCLEOTIDE SEQUENCE.  
 RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,  
 RA Chen Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,  
 RA Hsiung U.-N., Hsu C.-H., Huang J.-J., Han S.-Y., Hsiao S.-H.,  
 RA Hsiung U.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Liu H.-L.,

RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-N., Yu C.-Y., Yu S.-N.,  
 RA Wu H.-P., Shaw J.-F.;  
 RT "Oryza sativa BAC OJ1735\_C10 genomic sequence."  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC104284; AA04411.1; -; Genomic DNA.  
 DR EMBL: AC098832; AAT69581.1; -; Genomic DNA.  
 DR Gramene: Q6F357;  
 DR GO:0004806; F:triacylglycerol lipase activity; IEA.  
 DR GO:0006629; P:lipid metabolism; IEA.  
 DR InterPro: IPR002921; Lipase\_3.  
 DR InterPro: IPR008262; Lipase\_AS.  
 DR Pfam: PF01764; Lipase\_3; 1.  
 DR PROSITE: PS00120; LIPASE\_SER; UNKNOWN 1.  
 SQ SEQUENCE 407 AA; 43766 MW; F0FC2359EF0B4888 CRC64;

Query Match 31.0%; Score 740.5; DB 2; Length 407;  
 Best Local Similarity 37.5%; Pred. No. 4e-49;  
 Matches 163; Conservative 70; Mismatches 139; Indels 63; Gaps 7;

QY 17 WPELLGSNANAGLNPINDELRELLRCGDFCQVYTPFINDQSSYCGSSRYGKADLLH 76  
 DB 14 WREIHGSDSNGLDPDLDRSILSYGELVQATYDSFNRERSPHAGACVGHGDL- 72  
 QY 77 KTAFFPGADRFDDVAVYLYATATKSVVPEAF--LKSRREKMDRESNIGYVAVSNDETS 133  
 DB 73 AAGASAGSYATKFFYATSGLPVPEAFLLPLPLPSLLPAMSRRESNMGVAVATDEGV 132  
 QY 134 RVAGREVVYVNRGTCDYEWVDVLAQLESAPHLRTQOTTHVEKENEKKS IHKSSW 193  
 DB 133 AALGRDIVAMGTQVQSLWMIDMPVMPKGLR----- 166  
 QY 194 YDCENINLGSASAKDKGSDDDDDPK--VMQGMNTIYTSDEPKSPPTKLSARTOLQ 251  
 DB 167 -----VLGAAAA-----ANPRAIVHRGFLSVTSSKSKYKASARDVLE 208  
 QY 252 KLNQMTKYKDELTSTFAGSLGATLSVSAFDIYEN-----LTTELPTAVAV 300  
 DB 209 EVRLMELYKDEVTSLVYGHSLGALATLNAVDIVANGANCPASSSSQPCPTVAIV 268  
 QY 301 FGCPKVGNNKFFQOLFDSYPMLNVLHVRNVLDLPLVYKLMGVNIGLEIDSKSTFL 360  
 DB 269 FASPRVDDGFKAFAFSPDLRLALHVNAGDVMPVP--LGYDVAVKRLISTRSRPLY 326  
 QY 361 KDSKNPSDMNHLQALILHVSQGMHGVKGEFKVVKRSVALVNSCDFLKECELVPPAMVV 420  
 DB 327 RSPGTTETLHNECYLHGVAAGGEGAFKLAVERDVALLANKSYGALDKDTPVPRKVV 386  
 QY 421 QNKGMYLNGEYVLA 435  
 DB 387 KNRCMYVDADGHMAL 401

## RESULT 9

Q6RZ40\_ORYSA PRELIMINARY; PRT; 420 AA.

AC Q6RZ40;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Lipase-like.  
 GN Name=OJ159\_D09.27;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OC NCBI\_TaxID=39947;  
 RN NCBI\_TaxID=39947;  
 RP NUCLEOTIDE SEQUENCE.

RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
 RA Wu J., Nishimura Y., Cheng Z., Nagamura Y., Antonio B.A., Karamori H.,  
 RA Hosokawa S., Maekawa M., Arikawa K., Chiden Y., Hayashi M.,  
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,  
 RA Hijikita S., Honda M., Ichikawa Y., Ikonuma A., Iijima M., Ikeda M.,

RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,  
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
 RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,  
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K.,  
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,  
 RA Yano M., Jiang J., Gojobori T.;  
 RT "The genome sequence and structure of rice chromosome 1.";  
 RL Nature 420:312-316(2002).  
 DR EMBL; AP003792; BAB89211.1; -; Genomic\_DNA.  
 DR Gramene; Q8R240; -;  
 DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.  
 DR GO; GO:0006629; P:lipid metabolism; IEA.  
 DR InterPro; IPR002921; Lipase\_3.  
 DR InterPro; IPR008262; Lipase\_AS.  
 DR Pfam; PF01764; Lipase\_3; 1.  
 DR Pfam; PF01764; Lipase\_3; 1.  
 DR PROSITE; PS00120; LIPASE\_SER; UNKNOWN\_1.  
 DR PROSITE; PS00120; LIPASE\_SER; UNKNOWN\_1.  
 SQ SEQUENCE 420 AA; 45328 MW; 5915CC8680F5F2A0 CRC64;

Query Match 30.9%; Score 736; DB 2; Length 420;  
 Best Local Similarity 37.5%; Pred. No. 9,3e-49;  
 Matches 162; Conservative 69; Mismatches 141; Indels 60; Gaps 9;  
 QY 22 GSNAMAGLNPINDELRELLRCGDFCQVYDTFINDQSSYCGSSRYKADLHKTAFP 81  
 DB 31 GKDMGDLDPDLDRDRIIRYGELOATSDALIGDPASFPAGASRAAPAFRLKRA-A 89  
 QY 82 GGADRFDVAVLYATKAVSPEAFLLK--SRSREKMDRESNMIGYVVSNDSTSVAGRR 139  
 DB 90 SDPDAVYTRFVYATSSVRLPDAFWPBPAPSAAGAMSGESNMWGVAAADGVAAKAGRR 149  
 QY 140 EYVYVWRTCTDYENVVLGAQLBSAHLRTQCTTHVEKVENEKSIHKSMTDCNI 199  
 DB 150 DIVVAMRGTKRAVENANDLITLVADGV----- 179  
 QY 200 NLDSASKDKGSGDDDDDDPKVMQGMWITYTSEDPSPTKLSARTQLTKLQMTK 259  
 DB 180 -----GPGPGW-----TQPSVHRGFLSVYTSFSFSPFKLSARQVLAETRLIRA 226  
 QY 260 YKDETLSTFAGHSIGATLSVSAFDIVEN-----LTTEIPYAVVFGCPKVKNGKQ 312  
 DB 227 YKNECSITITIGHISGALSTLNAIDIVANGYNVWGSSRPVPYVALMALSPRVDDQFK 286  
 QY 313 QLPFSYPLNVLHVRNVLDLP-LYVYKMGVNIIGILELDSKSTFLKSKSPSDMN 371  
 DB 287 RAFPSTSNLSLRVNNAPDIVPTILPSAF--FKDVGAELVDTRRSPFLKDPAGPAQWNN 344  
 QY 372 LQALIHVVGSMHGVGE--FKVYVNRGSVALVNRKSCFLKEECVLPAMWVYONKQMTLN 428  
 DB 345 LECTYHAAVAGTGA-GDGAQFSLVVDRLALVNRKVDLRLDEYQVPAAMWEEKKMGYQN 403  
 QY 429 KDGWVLAPEE 440  
 DB 404 ASGRVTLQDHEE 415

RESULT 10  
 OSVP27 ORYSA PRELIMINARY; PRT; 418 AA.  
 ID OSVP27 ORYSA  
 AC OSVP27  
 DT 01-FEB-2005 (TREMBlrel. 29, Created)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)  
 DE Lipase-like protein.  
 GN Name=OJ1159 D09.22;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzoideae; Oryza.  
 OC NCBI\_TaxID=39947;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
 RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,  
 RA Hosokawa S., Maekawa M., Arikawa K., Chiden Y., Hayashi M.,  
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,  
 RA Hijioka S., Honda M., Ichioka Y., Idonuma A., Iijima M., Ikeda M.,  
 RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,  
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
 RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,  
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K.,  
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
 RA Yano M., Jiang J., Gojobori T.;  
 RT "The genome sequence and structure of rice chromosome 1.";  
 RL Nature 420:312-316(2002).  
 CC -1- CATALYTIC ACTIVITY: triacylglycerol + H(2O) = diacylglycerol + a  
 CC carboxylate.  
 DR EMBL; AP003792; BAB89211.1; -; Genomic\_DNA.  
 DR Gramene; Q5VP27; -;  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.  
 DR GO; GO:0016042; P:lipid catabolism; IEA.  
 DR InterPro; IPR002921; Lipase\_3.  
 DR InterPro; IPR008262; Lipase\_AS.  
 DR Pfam; PF01764; Lipase\_3; 1.  
 DR Pfam; PF01764; Lipase\_3; 1.  
 DR PROSITE; PS00120; LIPASE\_SER; UNKNOWN\_1.  
 DR PROSITE; PS00120; LIPASE\_SER; UNKNOWN\_1.  
 KW Hydrolyase; Lipid degradation.  
 SQ SEQUENCE 418 AA; 46822 MW; D484B9A38F9A62B5 CRC64;

Query Match 30.6%; Score 730; DB 2; Length 418;  
 Best Local Similarity 38.2%; Pred. No. 2,7e-48;  
 Matches 175; Conservative 51; Mismatches 158; Indels 74; Gaps 6;  
 QY 17 WPELGSNAMAGLNPINDELRELLRCGDFCQVYDTFINDQSSYCGSSRYKADLH 76  
 DB 5 WRELHSGHMDGLDPLDRCLTYGEMIMATYEAFIGEHSPPNAGACRYHADLFR 64  
 QY 77 K--TAFPGADRFPVAVLYATKAVSPEAFLLKSRREKMDRESNMIGYVVSNDSTSR 134  
 DB 65 RVDVSHPGW--YATRYIYATANADVHGVLLRLRCBGRATECNMGYVAAVTDGAA 121  
 QY 135 VAGREYVYVWRCGRDYENVVLGAQLBSAHLRTQCTTHVEKVENEKSIHKSMT 194  
 DB 122 ALGRDILVAMKRGORALEVADKLAPASAGL----- 156  
 QY 195 DCFNINLGSASKDKGSGDDDDDDPKVMQGMWITYTSEDPSPTKLSARTQ----- 248  
 DB 157 -----GPEGADGTDPVHRGYLSLTSEDOCSLKNQSHARMQNKLLGF 199  
 QY 249 -----LOTKLQMTKTKYDTELSTFAGHSLGATLSVSAFDIVEN----- 290  
 DB 200 DPMRQTLKQVLTETARLMDKXKBETSIYVIGSLGATLNLNADLAASVNTSSLSPS 259  
 QY 291 -TTEIPYAVVFGCPKVKNGKQFQOLFDSYPLNVLHVRNVLDLP-LYVYKMGVNIIGIE 349  
 DB 260 GETPAPYAVVFGSPRGDGRFRDLRLRLRNRPRDRIPHP--VGADVGE 317  
 QY 350 LEIDSRKSTFLKSKSPSDMNLTQALIHVVGSMHGVGEFKVYVNRGSVALVNRKSCFLKE 409  
 DB 318 LLITRLSPFLRRGSSSQSHDELCHLHGVAGMHDGRGFEVLVVDRLVALVNRKFDCLAD 377  
 QY 410 ECLVPLAMWVYONKQMTLNKDGENVLAPEEDPPEED 447  
 DB 378 EYVYVWRTCTDYENVVLGAQLBSAHLRTQCTTHVEKVENEKSIHKSMTDCNI 415

RESULT 11  
 OSVP27 ARATH PRELIMINARY; PRT; 527 AA.  
 ID OSVP27 ARATH  
 AC OSVP27  
 DT 01-FEB-2005 (TREMBlrel. 29, Created)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)  
 DE Lipase-like protein.  
 GN Name=OJ1159 D09.22;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzoideae; Oryza.  
 OC NCBI\_TaxID=39947;  
 RN [1]



DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)  
 DE Hypothetical protein F5D21.19 (A1951440/F5D21\_19).  
 GN Name=F5D21.19;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC Rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,  
 Maiti R., Rong C.M., Koo H., Fujii C.Y., Uterback T.R.,  
 RA Barstead M.E., Bowman C.L., White O., Nieman W.C., Fraser C.M.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Town C.D., Kaul S.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,  
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayaehizaki Y.,  
 RA Ishida J., Jiang P.X., Jones T., Kamuya A., Karlin-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,  
 RA Nguyen M., Onodera C.S., Palm C.J., Phan P.K., Quach H.L., Sakurai T.,  
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,  
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
 RA Ecker J.R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Kim C.J., Chen H., Cheuk R., Shin P., Bowser L., Carninci P.,  
 RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayaehizaki Y.,  
 RA Hsuan V.W., Ishida J., Jones T., Kamuya A., Karlin-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,  
 RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,  
 RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,  
 RA Yamada K., Yu G., Yuan S.C., Davis R.W., Theologis A., Ecker J.R.;  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a  
 CC carboxylate.  
 DR EMBL: AC024261; AAC52635.1; -; Genomic\_DNA.  
 DR EMBL: AF424572; ALU1566.1; -; mRNA.  
 DR EMBL: AY142023; AAM98287.1; -; mRNA.  
 DR PIR: F96552; F96552.  
 DR GO: GO:0016787; F:triacylglycerol lipase activity; IEA.  
 DR GO: GO:0016042; P:lipid catabolism; IEA.  
 DR GO: GO:0016042; P:lipid catabolism; IEA.  
 DR InterPro: IPR002921; Lipase\_3.  
 DR InterPro: IPR008262; Lipase\_AS.  
 DR InterPro: IPR00379; Ser\_estra.  
 DR Pfam: PF01764; Lipase\_3; 1.  
 DR PROSITE: PS00120; LIPASE\_SER; UNKNOWN 1.  
 KM Hydrolyase: Hypothetical protein, lipid degradation.  
 SQ SEQUENCE 527 AA; 60321 MW; 2161452f6c7f1a92 CkC64;  
 Query Match 29.5%; Score 703.5; DB 2; Length 527;  
 Best Local Similarity 35.5%; Pred. No. 4.4e-46;  
 Matches 168; Conservative 69; Mismatches 133; Indels 103; Gaps 14;  
 QY 17 WPBLGSNANAGLNPINDELRLRLRGDFQVYTFINDONSSTGSGRRYKADL-- 74  
 DB 91 WREVOGQNNWEGQLDPMMNHLRREIRYGEPAQACYSFDPSPSKYCGSGCKHPSPFL 150  
 QY 75 -----LHKTAFPGADPFDDVAVLYATAKVSVPAPFLKSRKMRKRESNIGVYVNS 129  
 DB 151 NLDLHLK-----GTTIRYVATSNINLEP-FFQKSLSSISWCHAMWGFVAVAT 201  
 QY 130 D--ETSVAGREVVYVWGTGRDYEWVDVLAOLDSAPHLRQOTTHVEKVENEEKS 187  
 DB 202 DEEVVSL-GRDVIAMRGVTYLVEM----- 228

QY 188 IHKSWYDFCNINMLGSASDKGSDDDDDPKVMQGMWITYTSDPKSPFTLSART 247  
 DB 229 -----YDL-----KDLCSANFGDDPSKIELGHDLTYTKEDSCKSFBSARE 272  
 QY 248 QLOTKLQMLTKYKDE---TLSTFAGHSLGATLVSVSAFDIVE-NL-----TTEIPV 296  
 DB 273 QVLAERVRLBYVTEBEGHKTSTVGHSLGASLALVSAVDIAELMLNHYPENNYKPI 332  
 QY 297 TAVFGCPKYGKKFQQLFPSYPMNLVLRNVLDLPLYPVKL----- 340  
 DB 333 TVFSFGSPRVGNLRFKRCDEL-GVKVLRVNVHDKVPSVPGIPTNKEFQOKVYEKTS 391  
 QY 341 --MGVYVIGELRIKDSKTFELKDSKNPSDMNLAITLVSGWGVKGE----FKVYVK 394  
 DB 392 PPMSTAVHGVGLADHKKSPFLKFTKDLGCANLEALHVDGTHGDEBAKFKCLVTK 451  
 QY 395 RSVALVYKSCDPLKECLVPPAMVWVQNKGVNLKDGWYL--APPEEDPTPE 445  
 DB 452 RDLALVYKSCDPLRGEYHVPFCWRQDENKGVNKGVGQGWTLPRRLLEPHGPE 504  
 RESULT 12  
 ID 004340 ARATH PRELIMINARY; PRT; 529 AA.  
 AC 004340;  
 DT 01-JUN-1997 (TReMBLrel. 04, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)  
 DE Putative lipase.  
 GN Name=At2G30550;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC Rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Town C.D., Haas B.J., Wu D., Maiti R., Hannick L.I., Chan A.P.,  
 RA Tallon L.J., Rooney T., Uterback T.R., Vanaken S.E., Feldblum T.V.,  
 RA White O., Fraser C.M.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Lin X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Town C.D., Kaul S.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=2208475; PubMed=12093376;  
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,  
 RA Feldmann K.A., Flavell R.B., White O., Salberg S.L.;  
 RT "Full-length messenger RNA sequences greatly improve genome  
 RT annotation.";  
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
 RA Feldmann K.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,  
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,  
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,  
 RA Carninci P., Chen H., Cheuk R., Hayaehizaki Y., Ishida J., Jones T.,  
 RA Kamuya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
 RA Meyer M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,  
 RA Sakurai T., Satou M., Seki M., Shin P., Southwick A., Shinozaki K.,  
 RA Davis R.W., Ecker J.R., Theologis A.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 NCLECTOTIDE SEQUENCE.  
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hsuan V.M.,  
 RA Lee J.M., Quach H.L., Tang C., Toriumi M., Wallender E.K., Wong C.,  
 RA Wu H.C., Yu G., Yuan S., Carninci P., Chen H., Cheuk R.,  
 RA Hayashizaki Y., Ishida J., Jones T., Kamuya A., Kawai J., Kim C.J.,  
 RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,  
 RA Shinn P., Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W.,  
 RA Ecker J.R., Theologis A., Trupp M.G., Wu T., Shinozaki K., Davis R.W.,  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a  
 CC carboxylate.  
 DR EMBL: U93215; AAB63082.2; -; Genomic\_DNA.  
 DR EMBL: AY086021; AAM63231.1; -; mRNA.  
 DR EMBL: AY091143; AAM14092.1; -; mRNA.  
 DR EMBL: AY142594; AAM13163.1; -; mRNA.  
 DR PIR: G84709; G84709.  
 DR GO: GO:0016787; F:hydrolyase activity; IEA.  
 DR GO: GO:0004806; F:triacylglycerol lipase activity; IEA.  
 DR GO: GO:0016042; P:lipid catabolism; IEA.  
 DR InterPro: IPR002921; Lipase\_3.  
 DR InterPro: IPR008262; Lipase\_AS.  
 DR InterPro: IPR00379; Ser\_estrs.  
 DR Pfam: PF01764; Lipase\_3; 1.  
 DR PROSITE: PS00120; LIPASE\_SER; UNKNOWN\_1.  
 DR Hydrolyase; lipid degradation.  
 KM SEQUENCE 529 AA; 60402 MW; 2F02B3C51953B020 CRC64;  
 SQ  
 Query Match 28.8%; Score 686.5; DB 2; Length 529;  
 Best Local Similarity 35.6%; Pred. No. 9.4e-45;  
 Matches 160; Conservative 78; Mismatches 133; Indels 79; Gaps 14;  
 QY 16 TWPELLGSNMAAGLNPINDELRELLRCGDFCVTYTFINDNSSYCGSSRYGKADLL 75  
 DB 104 TWKRIQGBDDWAGLMDPDLRLSELIRYGEQAQCYDAFDPDPASKYCGTSRTRELEFF 163  
 QY 76 HKTAFPGGADRFDVVAIYATATKAVSVEAFILKRSREKMDRESNMGYVAVSNDTSR 134  
 DB 164 DSL---GMIDSGYEVARLYATSNINLPN-FPSKSRMSKWSKANNMGYAVSDDETSR 219  
 QY 135 -VAGREVVVWRCGRDYENVVLYGAQLSAPHLLRTQOTTHVEKVENEEKSIHKSSW 193  
 DB 220 NRLGRDIAIAMRGVTLEWIALDKYLKPV-----TENKLR----- 257  
 QY 194 YDCFNINILGSASDKGSGDDDDDDPKVMQGMWTIYTSBPSPFKLSARTQLOTKL 253  
 DB 258 -C-----PDPAVKVBSGFLDLYTDKOTTCFKAFRSRQILTEV 295  
 QY 254 KQMTKYKD---TLSTFAGHSIGATLSVVSADPDI---NLTE---IPVTAVFGCP 304  
 DB 296 KRLVBEHDDDDSDSLITVTHSGLSGALAILSAVYIAEMRLNRSKGVIPVTAVLYGCP 355  
 QY 305 KVGKNGKFOQLFDSYFNINLVHVRVYDILPLYPVKMG-----YVNI 347  
 DB 356 RVGNVIRFERMEEL-GVAVLRVNVHVDVYPKSPGLFLNESRPHALMIAEGLPMCYSHVG 414  
 QY 348 IELIDSRKSTFLDKSKNPSDMHNLQATLHVSGMHGKGF-KVYVNRKSRVALVYKSCDF 406  
 DB 415 BELALDHQNSPFLKPSYVSTAHNLAMHLIDYHG-KGERFVLSSGRDHALVYKASDF 473  
 QY 407 LKEECLVPRAVWVQNGKAVLNKDGEMVLA 436  
 DB 474 LKEHQLIPFMRQDANKGMVNSSEGRWIOA 503  
 RESULT 13  
 Q9M9Y7\_ARATH PRELIMINARY; PRT; 515 AA.  
 AC Q9M9Y7\_ARATH PRELIMINARY; PRT; 515 AA.  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)

DE FAH5.11 protein (lipase, putative).  
 GN Name=FAH5.11; Synonyms=Atlg06800;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsie.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 NCLECTOTIDE SEQUENCE.  
 RA Federepiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,  
 RA Aliafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,  
 RA Gonzalez A., Kremetzkala I., Kim C., Lenz C., Li J., Liu S.,  
 RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,  
 RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.,  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 NCLECTOTIDE SEQUENCE.  
 RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,  
 RA Palm C.J., Bower L., Jones T., Banh U., Carninci P., Chen H.,  
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamuya A., Kawai J.,  
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakurai T.,  
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,  
 RA Ecker J., Theologis A., Davis R.W.,  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a  
 CC carboxylate.  
 DR EMBL: AC011001; AAF63138.1; -; Genomic\_DNA.  
 DR EMBL: AY095599; AAM20450.1; -; mRNA.  
 DR PIR: H86202; H86202.  
 DR GO: GO:0016787; F:hydrolyase activity; IEA.  
 DR GO: GO:0004806; F:triacylglycerol lipase activity; IEA.  
 DR GO: GO:0016042; P:lipid catabolism; IEA.  
 DR InterPro: IPR002921; Lipase\_3.  
 DR InterPro: IPR008262; Lipase\_AS.  
 DR InterPro: IPR00379; Ser\_estrs.  
 DR Pfam: PF01764; Lipase\_3; 1.  
 DR PROSITE: PS00120; LIPASE\_SER; UNKNOWN\_1.  
 DR Hydrolyase; lipid degradation.  
 KM SEQUENCE 515 AA; 58445 MW; DD59442CB9166451 CRC64;  
 SQ  
 Query Match 28.1%; Score 670; DB 2; Length 515;  
 Best Local Similarity 35.1%; Pred. No. 1.7e-43;  
 Matches 157; Conservative 73; Mismatches 141; Indels 76; Gaps 12;  
 QY 16 TWPELLGSNMAAGLNPINDELRELLRCGDFCVTYTFINDNSSYCGSSRYGKADLL 75  
 DB 88 TWKRIQGBDDWAGLMDPDLRLSELIRYGEQAQCYDAFDPDPASKYCGTSRTRELEFF 147  
 QY 76 HKTAFPGGADRFDVVAIYATATKAVSVEAFILKRSREKMDRESNMGYVAVSNDTSR 134  
 DB 148 DSLGIIDSG--YEVARLYATSNINLPN-FPSKSRMSKWSKANNMGYAVSDDETSR 204  
 QY 135 V-AGREVVVWRCGRDYENVVLYGAQLSAPHLLRTQOTTHVEKVENEEKSIHKSSW 193  
 DB 205 CRLGRDIAIAMRGVTLEWIALDKYLKPV-----SGNG 240  
 QY 205 CRLGRDIAIAMRGVTLEWIALDKYLKPV-----SGNG 240  
 DB 205 CRLGRDIAIAMRGVTLEWIALDKYLKPV-----SGNG 240  
 QY 194 YDCFNINILGSASDKGSGDDDDDDPKVMQGMWTIYTSBPSPFKLSARTQLOTKL 253  
 DB 241 PRC-----PDPAVKVBSGFLDLYTDKOTTCFNFSRQILTEV 280  
 QY 254 KQMTKYKD---TLSTFAGHSIGATLSVVSADPDI---NLTE---IPVTAVFGCP 304  
 DB 281 KRLVBEHDDSDSLITVTHSGLSGALAILSAVYIAEMRLNRSKGVIPVTAVLYGCP 340  
 QY 305 KVGKNGKFOQLFDSYFNINLVHVRVYDILPLYPVKMG-----YVNI 347  
 DB 341 RVGNVIRFERMEEL-GVAVLRVNVHVDVYPKSPGLFLNERAPOLMIAEGLPMCYSHVG 399  
 QY 348 IELIDSRKSTFLDKSKNPSDMHNLQATLHVSGMHGKGF-KVYVNRKSRVALVYKSCDF 407  
 DB 400 EMLLDHNSPFLKPSYVSTAHNLAMHLIDYHGKGFVLSGSDPALVYKASDFL 459  
 QY 408 KEECLVPRAVWVQNGKAVLNKDGEMV 434

Db 460 KDHFMVPPYWRQDANKGMVNTDGRW1 466

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RESULT 14
082274_ARATH PRELIMINARY; PRT; 355 AA.
ID 082274
AC 082274
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Putative lipase.
GN Name=At2g31100;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rounseley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Romling C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005311; AAC63840.1; -; Genomic_DNA.
DR PIR; E84716; E84716.
DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR002921; Lipase_3.
DR InterPro; IPR008262; Lipase_AS.
DR Pfam; PF01764; Lipase_3; 1.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
SQ SEQUENCE 355 AA; 40471 MW; 18CE5655DFCE4C7 CRC64;

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Query Match 25.8%; Score 616; DB 2; Length 355;  
 Best Local Similarity 32.9%; Pred. No. 1.7e-39;  
 Matches 146; Conservative 69; Mismatches 111; Indels 118; Gaps 8;

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Qy 17 WPEILGSNAAGLNPINDELRELLRCGDFCQVYTFINDQSSYSGSSRYKADLLH 76
Db 9 WKELSSGSKKKDLDPDLDRRIIHYGDMAEI-----AATPKSSLLS 54
Qy 77 KTAAPGADRPDVAVIYATKASVPEAFILKSRREKMRRESNMIGYVVVSNDETSRA 136
Db 55 P-----VTSKPTL-----SDEGKKLL 70
Qy 137 GRREVVVVRGTCRDYEMVDVIGAOLESAPHLARTQOTTHVEKENEKKSIIHSSWYDC 196
Db 71 GRKGIIVAMGTTQLYEMADDFPLESA----- 99
Qy 197 FNILLSASAKDKGSDDDDDPKYMGWMTIYTSDEPKSPFTKLARTQOTKLKQL 256
Db 100 --WVFFGCA-----NNDPRVANGWLSLSTDPKSRDTSKSAQOVBEELKRL 147
Qy 257 MTXYKDETLITFAGSLGATLSVSAFDIVEN-----LTTEIPYAVVFCGPRVGN 308
Db 148 LELYKNEDVITTLTGHSLGAVMSILSADFLHNEMPKITPLOSLSLCTVPAFGSPQIGD 207
Qy 309 KKRPQQLFDSYPNLVNLRVNYIDILPLYVGLMKYVNIIGILELIDSKRSTLKSKSPSD 368
Db 208 RSPFRVLSELEHLILRVTVNPDLIPRPV--FRPTDIGELQINTLKSSEVLKSLNLGH 265
Qy 369 WHNLQALILVVGSGHGVGFEKPVNKRVSVALVNSCDFLKEECVPPAMVWVQKGMVNLN 428
Db 266 FHNLEALIHGVAAGTQHNQGEFKLEINRDIALVNGGLALEBKYLIVPGHMVLEHKMVGVS 325
Qy 429 KDGEMVL-----APPEEDPTPE 445
Db 326 DDGTWKLNGDRSKKKQGEDEKEE 349

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RESULT 15
09C8G6_ARATH PRELIMINARY; PRT; 529 AA.
ID 09C8G6
AC 09C8G6
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Lipase, putative.
GN Name=AtK2.3;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC rosids; euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Romling C.M., Koo H., Fujii C.Y., Utecherback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2O) = diacylglycerol + a
CC carboxylate.
DR EMBL; AC025295; AAG51101.1; -; Genomic_DNA.
DR PIR; A86428; A86428.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR002921; Lipase_3.
DR InterPro; IPR008262; Lipase_3.
DR InterPro; IPR00379; Ser esters.
DR Pfam; PF01764; Lipase_3; 1.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
DR Hydrolyase; lipid degradation.
SQ SEQUENCE 529 AA; 60742 MW; BA21D67856CD097E CRC64;

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Query Match 25.4%; Score 606.5; DB 2; Length 529;  
 Best Local Similarity 32.0%; Pred. No. 1.6e-38;  
 Matches 151; Conservative 79; Mismatches 157; Indels 85; Gaps 15;

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Qy 1 MAEAOPLGSKGKPTPEILGSNAAGLNPINDELRELLRCGDFCQVYTFINDQ 60
Db 104 MTPAASP--REKISKMRRLGSSNMENLLDPLHPMLRRVTKGGEVESVYSLDPL 161
Qy 61 SSYCGSSRYKADLLHKTAPFGADR--FDVAVLYATKASVPEAFILKSRREKMDRE 118
Db 162 SEFGSSRYNRNKLFEEL---GLTRHGYVTYKIYMSRVDPQW--LSALGETWSKD 216
Qy 119 SNMIGYVVVSNDETSRVAAGREVVVVRGTCRDYEMVDVIGAOLESAPHLARTQOTTHVE 178
Db 217 SNMNGFVAVAGDRESLALIGRDIYAVRGTVTFEMFMDLRTSMEP----- 262
Qy 179 KVENEKKSIIHKSWMYDGFNINLIGSASKGKSDDDDDDDPKYMGWMTIYTSDEPKS 238
Db 263 -----FDC-----EGK-----HGKTVVVGQGFSLYNSKSELT 291
Qy 239 PFTKLARTQOTKLKQIMTKYD--ETLSTFAGSLGATLSVSAFDIVENLTTEIP- 295
Db 292 RINKESASEQTMDEVKLVNPFKDRGEVSLITTHSLGALALMAYEAR---DVFA 347
Qy 296 ---VTAVFECGCPVGNKKFQQLFDSYPNLVNLRVNYIDILPLYP---VKLMG----- 342
Db 348 LSGNISVTSFGARVGNLAFKELNSL--GVKVLRVVVKQDIPVPLGIVENKVLNKLNPI 406
Qy 343 -----YVNIIGILELIDSKRSTFLKDSKNPSDMHNLQALILVVGSGHGVGFEKPVNKR 395
Db 407 TSLNMYIRHVYGTQLKLDVSSPYVKRSDLGRAHNLVLYLHVDGPHRKKSQGFVAVAR 466
Qy 396 SVALVNSCDFLKEECVPPAMVWVQKGMVNLND--GEVY--LAPPEEDPTPE 444

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Db 467 DVASVNRKSTMDLIDLRLRIPFPMYQVAHKGILINKQGRWVXKVRAPEDIPSP 518

Search completed: December 22, 2005, 19:42:26  
Job time : 151.5 secs



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Query Match          4.9%; Score 116; DB 6; Length 278;
Beet Local Similarity 21.5%; Pred. No. 0.0024;
Matches 60; Conservative 42; Mismatches 117; Indels 60; Gaps 11;

Oy 121 WIGYVWVSNDESHVAGRREYVWVWVGTCDYEMVVDLGAQLSAPHLRTQOTTHVEKY 180
Db 13 WVQYAAATYCCNNVVAADGEKLNCSVNCND---VEAGSTVLSFSDDTITDTAGFAV 69
Oy 181 ENEEKSIHSSWYDCFNINILGSAKDKGSGDDDDDDPKMGGMN--IYSEDP-- 236
Db 70 DNTKKAIV-----VAFRGSYS-----IRMWVIDATFPQTFGL 102
Oy 237 ----KSPTKLSA-----RTQLQFTLKQMTKRYNDETLSTFAGHSIGATLVSAFDIYE 288
Db 103 CDGCKAELEGFWTAKNVVRDRIITKLDELKPEHSD--KYIVVGHSGIAAIASTAAADL-- 158
Oy 289 NLATTEIPYAVAFCCPKVGNKKFQOLPDSYPNVLVHRNVIDLIPYPKLMGVYNI 348
Db 159 -RTGNVDAILVAVAPRVANKPLAEFITNGN-NYRFTN-DDEPVKPLPLTMGYHISF 215
Oy 349 ELEIDSRKSTPLDKSNKPSDMHNLQAILHVSGHGKYG 387
Db 216 EYITAPDNTTITVDNQ-----VTVLGDGVNPKG 243

RESULT 3
US-10-495-597-11
; Sequence 11, Application US/10495597
; Publication No. US20050255544A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Vind, Jesper
; APPLICANT: Heide-Hansen, Hans Peter
; APPLICANT: Erlandsen, Lise
; TITLE OF INVENTION: LipoLytic Enzyme Variants and Method for their Production
; FILE REFERENCE: 10248-204-US
; CURRENT APPLICATION NUMBER: US/10/495,597
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: PCT/DK03/00028
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/353,557
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: DK 2002 00074
; PRIOR FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2

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RESULT 4
US-10-495-597-14
; Sequence 14, Application US/10495597
; Publication No. US2005025544Al
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Vind, Jesper
; APPLICANT: Heldt-Hansen, Hans Peter
; APPLICANT: Erlandsen, Luise
; TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production
; FILE REFERENCE: 10248.204-US
; CURRENT APPLICATION NUMBER: US/10/495,597
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: PCT/DK03/00028
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/353,557
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: DK 2002 00074
; PRIOR FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Thermomyces lanuginosus
US-10-495-597-14

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Query March 4.64; Score 110.5; DB 6; Length 269;
Best Local Similarity 25.24; Prod. No. 0.0072;
Matches 28; Conservative 22; Mismatches 56; Indels 5; Gaps 2;

Qy 244 SARTLOTKTKOMTKYKDETLTITFAGSLGATLSVSAPIVENTTTEIPTVAVFGC 303
      | : : : : : ||||| : : : : :
Db 119 SVADTLRQKEDAVREHPD--YRVVFTGSLGALATVAGADLRG--GYDIDVRSYA 173
      | : : : : : ||||| : : : : :

Qy 304 PKYGNKFFQOLPDSYPNLNTLAVRNVIDLPLYVVKMGVNIQIELEIDS 354
      | : : : : : ||||| : : : : :
Db 174 PRVGNRAFAEFLVYQTGGTLRYRTTHNDIYVRLPRPFGYSSPEYWIKS 224

RESULT 5
US-10-495-597-12
; Sequence 12, Application US/10495597
; Publication No. US20050255544A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Wind, Jesper
; APPLICANT: Heldt-Hansen, Hans Peter
; APPLICANT: Erlandsen, Baise
; TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production

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FILE REFERENCE: 10248.204-US  
CURRENT APPLICATION NUMBER: US/10/495,597  
CURRENT FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: PCT/DK03/00028  
PRIOR FILING DATE: 2003-01-16  
PRIOR APPLICATION NUMBER: US 60/353,557  
PRIOR FILING DATE: 2002-02-04  
PRIOR APPLICATION NUMBER: DK 2002 00074  
PRIOR FILING DATE: 2002-01-16  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 12  
LENGTH: 270  
TYPE: PRT  
ORGANISM: Aspergillus niger  
US-10-495-597-12

Query Match 4.5%; Score 108; DB 6; Length 270;  
Best Local Similarity 30.9%; Pred. No. 0.012;  
Matches 29; Conservative 16; Mismatches 41; Indels 8; Gaps 4;

Qy 244 SARQLOTKLKQMTKYDELTSTFAGHSGLATLSVSAFDIVENTTEIPYAVVFGC 303  
Db 119 AAADNLTSKIKSAMSTVSGYTL--YFTGHSGLGALATLGA-TVLRN--DGYSVELYTYGC 173  
Qy 304 PKVGNKKFQOLFDSY---PNIIVLHVNRVIDLI 334  
Db 174 PRVGNVALAEHITSGSGANFPVTHNDIVPRVP 207

RESULT 6  
US-10-495-597-4  
Sequence 4, Application US/10495597  
Publication No. US20050255544A1  
GENERAL INFORMATION:  
APPLICANT: Svendsen, Allan  
APPLICANT: Vind, Jesper  
APPLICANT: Heidt-Hansen, Hans Peter  
APPLICANT: Erlandsen, Luise  
TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production  
FILE REFERENCE: 10248.204-US  
CURRENT APPLICATION NUMBER: US/10/495,597  
CURRENT FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: PCT/DK03/00028  
PRIOR FILING DATE: 2003-01-16  
PRIOR APPLICATION NUMBER: US 60/353,557  
PRIOR FILING DATE: 2002-02-04  
PRIOR APPLICATION NUMBER: DK 2002 00074  
PRIOR FILING DATE: 2002-01-16  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 4  
LENGTH: 270  
TYPE: PRT  
ORGANISM: Rhizopus oryzae  
US-10-495-597-4

Query Match 4.3%; Score 101.5; DB 6; Length 270;  
Best Local Similarity 28.6%; Pred. No. 0.047;  
Matches 28; Conservative 18; Mismatches 45; Indels 7; Gaps 3;  
Qy 264 TLSTFPGHSGLATLSVSAFDIVENTTEIPYAVV--GCPVGNKKFQOLFDS--YR 319  
Db 137 TYKIVTGHSLGAGQALLAGDLVOREPRLSPKMLSTFVGSPVGNFTFAYVESGICP 196  
Qy 320 NNLVHVNRVIDLIPLYPVKLMGYVNICIELEIDSRSK 357  
Db 197 FQRTVHKR---DIVPHVDPQSGFLHPRVESMIKSGS 231

RESULT 7  
US-10-495-597-13  
Sequence 13, Application US/10495597

Publication No. US20050255544A1  
GENERAL INFORMATION:  
APPLICANT: Svendsen, Allan  
APPLICANT: Vind, Jesper  
APPLICANT: Heidt-Hansen, Hans Peter  
APPLICANT: Erlandsen, Luise  
TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production  
FILE REFERENCE: 10248.204-US  
CURRENT APPLICATION NUMBER: US/10/495,597  
CURRENT FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: PCT/DK03/00028  
PRIOR FILING DATE: 2003-01-16  
PRIOR APPLICATION NUMBER: US 60/353,557  
PRIOR FILING DATE: 2002-02-04  
PRIOR APPLICATION NUMBER: DK 2002 00074  
PRIOR FILING DATE: 2002-01-16  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 13  
LENGTH: 269  
TYPE: PRT  
ORGANISM: Aspergillus niger  
US-10-495-597-13

Query Match 4.1%; Score 98; DB 6; Length 269;  
Best Local Similarity 19.9%; Pred. No. 0.096;  
Matches 52; Conservative 39; Mismatches 92; Indels 78; Gaps 9;

Qy 100 SVPEAFILKRSRREKWD--RES---NWIGYVVSNDTSRVAGREVVYVMRTCDYE 153  
Db 36 SVGNCPLEVAASQTSLDEFNNESSYGNPAGYLA--DETNYL-----LVISFRGSADLAN 88  
Qy 154 WVDVIGAGQLESANHLATQOTTHHEKVENEKSIIHSSWYDCFNINILGSASDKXGGS 213  
Db 89 WVANLNFGLDASDLCSGCE-----VHSGFW----- 114  
Qy 214 DDDDDDDPKWQGMWITTSDEPKSPPTKLARSOTQTKLQMTKYDELTSTFAGHS 273  
Db 115 -----KAMSELAFT-----ISKYSBALSBSHSDVSLVLT--GHS 146  
Qy 274 LGATLSVSAFDIVENTTEIPYAVVFGCPKVGNNKKFQOLFDSYPNILVHVNRVIDLI 333  
Db 147 YGALLALALATATL---BNSGSELVLYVYGQPRIGNEALATYITDQNGKGNVRVTHNDIV 203  
Qy 334 PLYPVKLMGYVNICIELEIDS 354  
Db 204 PKLPPTLGYHHSPEYIYSS 224

RESULT 8  
US-10-495-597-1  
Sequence 1, Application US/10495597  
Publication No. US20050255544A1  
GENERAL INFORMATION:  
APPLICANT: Svendsen, Allan  
APPLICANT: Vind, Jesper  
APPLICANT: Heidt-Hansen, Hans Peter  
APPLICANT: Erlandsen, Luise  
TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production  
FILE REFERENCE: 10248.204-US  
CURRENT APPLICATION NUMBER: US/10/495,597  
CURRENT FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: PCT/DK03/00028  
PRIOR FILING DATE: 2003-01-16  
PRIOR APPLICATION NUMBER: US 60/353,557  
PRIOR FILING DATE: 2002-02-04  
PRIOR APPLICATION NUMBER: DK 2002 00074  
PRIOR FILING DATE: 2002-01-16  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 1  
LENGTH: 265  
TYPE: PRT

ORGANISM: Absidia reflexa  
US-10-495-597-1

Query Match 4.1%; Score 97.5; DB 6; Length 265;

Best Local Similarity 24.3%; Pred. No. 0.1;

Matches 35; Conservative 26; Mismatches 56; Indels 27; Gaps 6;

QY 222 KVMGMMTIYTSBDPKSPFTLSARTQTKLKQMLTKYKDETLSTPAGSLGATLSV 281  
DB 108 KVMGMMTIYTSBDPKSPFTLSARTQTKLKQMLTKYKDETLSTPAGSLGATLSV 154  
QY 282 SAPDIVENTLTPYAVVFCGCPKVGKPKFOO--LFDSYPMNLAVHVNIDLPLYPVK 339  
DB 155 SALLVHNGHANIEI--YTGQSPRIGTGFANVYIGTKIPYQRLVHER--DIVPHLPPG 209  
QY 340 LMGVNIIGIELEIDSRKSTFLKDS 363  
DB 210 AFGFLHAGEEPMI-----MKDS 226

## RESULT 9

US-10-495-597-6

Sequence 6, Application US/10495597

Publication No. US20050255544A1

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: Heide, Jesper

APPLICANT: Heide, Hansen, Hans Peter

TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production

FILE REFERENCE: 10248.204-US

CURRENT APPLICATION NUMBER: US/10/495,597

CURRENT FILING DATE: 2004-05-14

PRIOR APPLICATION NUMBER: PCT/DK03/00028

PRIOR FILING DATE: 2003-01-16

PRIOR APPLICATION NUMBER: US 60/353,557

PRIOR FILING DATE: 2002-02-04

PRIOR APPLICATION NUMBER: DK 2002 00074

PRIOR FILING DATE: 2002-01-16

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn version 3.2

SEQ ID NO 6

LENGTH: 312

TYPE: PRT

ORGANISM: Aspergillus tubingensis

US-10-495-597-6

Query Match 4.1%; Score 97; DB 6; Length 312;

Best Local Similarity 21.1%; Pred. No. 0.15;

Matches 53; Conservative 40; Mismatches 70; Indels 88; Gaps 12;

QY 123 GYVVNSNETSVAVAGREYVYVWGTGCRDYEVNDVGLAQLESANHLTLTQOTTHVEKEN 182  
DB 103 GY--VATDSS-----KEITVFRGTGSD-----TNQLDTNYTL-----TPDTPLPQ 143  
QY 183 EEKKSIIHSSWDCFNINILGSASKDKGSDDDDDDDPKVQGMNTIYTSBDPKSPFTK 242  
DB 144 CNSCEVHGGYI-----GN----- 157  
QY 243 LSARTQTKLKQMLTKYKDETLSTPAGSLGATLSVVSAPDIVENTLTPYAVVFCG 302  
DB 158 ISVQGVSVLQGVQSGPFDVLTVT--GHSLGASLALTAAGL--SATYONIRLTYFG 212  
QY 303 CPKVGKPKFOOLFDSYPM-----LNLVHVNVDLPLYPVKLMGVNIIGIELE-E 351  
DB 213 EP-----KSNQAFASYMDAFQASSPDTTQYFRVTHANDGIPNLPRADEGAHVVEYWS 267  
QY 352 ID--SRKSTFL 360  
DB 268 VDPYSAQNTFV 278

RESULT 10

US-10-770-726-77

Sequence 77, Application US/10770726

Publication No. US20050266409A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Brown, Eugene

APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING

FILE REFERENCE: AM101079 (031896-010000)

CURRENT APPLICATION NUMBER: US/10/770,726

CURRENT FILING DATE: 2004-02-04

NUMBER OF SEQ ID NOS: 48640

SOFTWARE: PatentIn version 3.2

SEQ ID NO 77

LENGTH: 4128

TYPE: PRT

ORGANISM: Homo sapiens

US-10-770-726-77

Query Match 3.9%; Score 94; DB 6; Length 4128;

Best Local Similarity 21.1%; Pred. No. 9.6;

Matches 96; Conservative 54; Mismatches 150; Indels 156; Gaps 23;

QY 80 FPGGADRFVAVLYATATK---VSVEAPFLKSRSEKMDRESNMIGYVVNSNETSRV 135  
DB 1729 FPGGADRFVAVLYATATK---VSVEAPFLKSRSEKMDRESNMIGYVVNSNETSRV 180  
QY 136 AGREVVYVWGTGCRDYEVNDVGLAQLESANHLTLTQOTTHVEKENEEKSIHSSWYD 195  
DB 1781 SFRR--IARRGSC---VTQVGL-LESVYEMR-----KODPRLSTKQSFVD 1821  
QY 196 CFNINILGSASKDKGSDDDDDDDPKVQGMNTIYTS--EDPKSPFTKLSARTQTKL 253  
DB 1822 RSLITLHRCGLD-----ALREFFSITVDAIDVLKSRFTKLNESF--PDTQI 1867  
QY 254 KQMLTKYKDETLSTPAGSLGATLSVVSAPDIVENTLTPYAVVFCGCPKVGKPKFOO--LFDSYPMNLAVHVN 288  
DB 1668 TKKGGYK--ILDVWYSLRPDGVHAKESKINGVHSGSCITEGNETLTKLTCYDAFTE 1925  
QY 289 NLUTE-----TPYAVVFCGCPKVGKPKFOO--LFDSYPMNLAVHVN 328  
DB 1926 NMAGENQLERRRLYHCAVNCALSVICVF---NELKPYQGLPSEKPEKNLLIFEN 1980  
QY 329 VIDLPLYPVKLMGVNIIGIELEID--SRKSTFLK-----DSKNPSDMHNL----- 372  
DB 1981 LIDLKRY-----NPPVAVEVPMERKKYIIRKREAREANAGSDGDPYMSLSGLYA 2032  
QY 373 -----QAILHVVSGMHGKGEFKVNNKRSVA---LVNKSDFL-KEE 410  
DB 2033 DSTLSEMSQPDFSTGVSYSSQDPRPAPGRFRRRERQDPVTYHDDVLEMDLNRHE 2092  
QY 411 CLVPRAMVYVQNKGMVNLKQGEWTLAP--BEDTTP 444  
DB 2093 CMARPLT-----ALVKHMRSLGPPQGEEDSV 2119

RESULT 11  
US-10-495-597-2  
Sequence 2, Application US/10495597  
Publication No. US20050255544A1  
GENERAL INFORMATION:  
APPLICANT: Svendsen, Allan  
APPLICANT: Wind, Jesper  
APPLICANT: Heide, Hansen, Hans Peter  
TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production  
FILE REFERENCE: 10248.204-US  
CURRENT APPLICATION NUMBER: US/10/495,597  
CURRENT FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: PCT/DK03/00028  
PRIOR FILING DATE: 2003-01-16  
PRIOR APPLICATION NUMBER: US 60/353,557



V--- 102

```

Qy 273 SLGATLSVSAFDIVENTTEIPVTAVVFGCPKVGKFKQOLPDSYPNLNLVAVR-----N 328
Db 103 ---LNLRTQRPFOVYLKMETQM-----KGLKAKFRJEDDRKLTMLMKHQLKEX 149
Qy 329 VIDILIPVYKLMGVNIGILEIDSRKSTPLKDSKNPSDMHNLQAILHVVSQMHGVKGE 388
Db 150 MDELPLPLPV-LEQY-----KTDAKLITQFKE-----EIRNLSAVLTGIOEBIGAY-D 195
Qy 389 FKVVNKSVALVNSCDFLKE-EC-----LVPRAMVVQNGKMWLNKDGENVLAP 437
Db 196 YEEHLQVRVLSLETRLRDCMKKLTGCKLMKITGPV--TVKTSG---TRFGAMWMDP 245

```

# RESULT 14

```

US-11-174-150-27
; Sequence 27, Application US/11174150
; Publication No. US20050260714A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Ritvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50022
; CURRENT APPLICATION NUMBER: US/11/174,150
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/257,174
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: PCT/US01/11797
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/196,603
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/199,417
; PRIOR FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-174-150-27

```

```

Query Match 3.7%; Score 87.5; DB 7; Length 478;
Best Local Similarity 22.1%; Pred. No. 1.9; Indels 55; Gaps 13;
Matches 52; Conservative 43; Mismatches 85;
Qy 221 PKVMQGMNTIYSEDPK-----SPTKLSARTOLQTKLQMLTKYKDETLSTTFAGH 272
Db 48 PK--EGWQVYSAQDPDRKICTVAFPGNLCSRDASKRQLRLLEKVNMSQSIEV--- 102
Qy 273 SLGATLSVSAFDIVENTTEIPVTAVVFGCPKVGKFKQOLPDSYPNLNLVAVR-----N 328
Db 103 ---LNLRTQRPFOVYLKMETQM-----KGLKAKFRJEDDRKLTMLMKHQLKEX 149
Qy 329 VIDILIPVYKLMGVNIGILEIDSRKSTPLKDSKNPSDMHNLQAILHVVSQMHGVKGE 388
Db 150 MDELPLPLPV-LEQY-----KTDAKLITQFKE-----EIRNLSAVLTGIOEBIGAY-D 195
Qy 389 FKVVNKSVALVNSCDFLKE-EC-----LVPRAMVVQNGKMWLNKDGENVLAP 437
Db 196 YEEHLQVRVLSLETRLRDCMKKLTGCKLMKITGPV--TVKTSG---TRFGAMWMDP 245

```

```

RESULT 15
US-10-495-597-10
; Sequence 10, Application US/10495597
; Publication No. US20050255544A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Vind, Jesper
; APPLICANT: Heldt-Hansen, Hans Peter

```

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; APPLICANT: Erlandsen, Luise
; TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production
; FILE REFERENCE: 10248.204-US
; CURRENT APPLICATION NUMBER: US/10/495,597
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: PCT/DK03/00028
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/353,557
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: DK 2002 00074
; PRIOR FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Penicillium camemberti
US-10-495-597-10

```

```

Query Match 3.6%; Score 87; DB 6; Length 278;
Best Local Similarity 24.4%; Pred. No. 0.99;
Matches 29; Conservative 24; Mismatches 58; Indels 8; Gaps 4;
Qy 246 RTQLQTLKQMLTKYKDETLSTTFAGHSLGATLSVSAFDIVENTTEIPVTAVVFGCPK 305
Db 120 RDIILKELKEVVA--QNPVYELVVVGHSLGAAVATLATDLRGKGYPSAKLYA--YASPR 175
Qy 306 VGKFKFOQLPDSY--PNLNLVHVRNVIDLIPVYKLMGVNIGILEIDSRKSTFLKDS 363
Db 176 VGNALAKYITTAQNNRPFHTN---DPVRKPLLSMGYHVSPEVWITSNNATVSTS 231

```

Search completed: December 22, 2005, 19:53:13  
Job time : 9 secs



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Qy 301 FGCPRVGNKKFQQLFDSYPNLNVLHVRNVIDLIPYVKLMGYVNIIELEIDSRKSTFL 360
Db 301 FGCPRVGNKKFQQLFDSYPNLNVLHVRNVIDLIPYVKLMGYVNIIELEIDSRKSTFL 360
Qy 361 KDSKNPSPDMHNLQAILHVVSGMHGKGFVKVYKRSVALVYKSCDFLKEECLVPPAMVV 420
Db 361 KDSKNPSPDMHNLQAILHVVSGMHGKGFVKVYKRSVALVYKSCDFLKEECLVPPAMVV 420
Qy 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447
Db 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447

RESULT 2
US-10-674-540-11
; Sequence 11, Application US/10674540
; Publication No. US20040158891A1
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 1079-10
; CURRENT APPLICATION NUMBER: US/10/674,540
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Plant
; US-10-674-540-11

Query Match 99.7%; Score 2377; DB 4; Length 447;
Best Local Similarity 99.8%; Pred. No. 2,1e-216; Indels 0; Gaps 0;
Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAABEOPGLSKPGTPELIGSNMAGLNPDLNDELRELLRCGDFCQVYTFINDQNSYCGSSRYGKADL 60
Db 1 MAABEOPGLSKPGTPELIGSNMAGLNPDLNDELRELLRCGDFCQVYTFINDQNSYCGSSRYGKADL 60
Qy 61 SSYCGSSRYGKADLHKTAFPGADRFDVAVLYATAKVSPEAFLLKRSREKMDRESN 120
Db 61 SSYCGSSRYGKADLHKTAFPGADRFDVAVLYATAKVSPEAFLLKRSREKMDRESN 120
Qy 121 WIGYVVSNDSTSRVAGREYVYVWRCRCRDYEWVDVYGAQLESAPHLRTQOTTTHVEKV 180
Db 121 WIGYVVSNDSTSRVAGREYVYVWRCRCRDYEWVDVYGAQLESAPHLRTQOTTTHVEKV 180
Qy 121 WIGYVVSNDSTSRVAGREYVYVWRCRCRDYEWVDVYGAQLESAPHLRTQOTTTHVEKV 180
Db 121 WIGYVVSNDSTSRVAGREYVYVWRCRCRDYEWVDVYGAQLESAPHLRTQOTTTHVEKV 180
Qy 181 ENEEKKS1HKSSWYDCFNINILGASAKDKGSDDDDDDDPKVMQGMWTIYTSSEDPKSPF 240
Db 181 ENEEKKS1HKSSWYDCFNINILGASAKDKGSDDDDDDDPKVMQGMWTIYTSSEDPKSPF 240
Qy 181 ENEEKKS1HKSSWYDCFNINILGASAKDKGSDDDDDDDPKVMQGMWTIYTSSEDPKSPF 240
Db 181 ENEEKKS1HKSSWYDCFNINILGASAKDKGSDDDDDDDPKVMQGMWTIYTSSEDPKSPF 240
Qy 241 TKLSARTOLOTKLQKLMTKYKDELTSTFAGHSLGATLSVVSAPDIVENLTTEIPVTAVV 300
Db 241 TKLSARTOLOTKLQKLMTKYKDELTSTFAGHSLGATLSVVSAPDIVENLTTEIPVTAVV 300
Qy 301 FGCPRVGNKKFQQLFDSYPNLNVLHVRNVIDLIPYVKLMGYVNIIELEIDSRKSTFL 360
Db 301 FGCPRVGNKKFQQLFDSYPNLNVLHVRNVIDLIPYVKLMGYVNIIELEIDSRKSTFL 360
Qy 361 KDSKNPSPDMHNLQAILHVVSGMHGKGFVKVYKRSVALVYKSCDFLKEECLVPPAMVV 420
Db 361 KDSKNPSPDMHNLQAILHVVSGMHGKGFVKVYKRSVALVYKSCDFLKEECLVPPAMVV 420
Qy 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447
Db 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447
```

```
Db 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447

RESULT 3
US-10-424-599-153165
; Sequence 153165, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 153165
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: PAT_MRT3847_109332C.1.pep
; US-10-424-599-153165

Query Match 54.9%; Score 1310; DB 4; Length 419;
Best Local Similarity 58.1%; Pred. No. 3e-116;
Matches 251; Conservative 54; Mismatches 99; Indels 28; Gaps 3;

Qy 15 PTWPELIGSNMAGLNPDLNDELRELLRCGDFCQVYTFINDQNSYCGSSRYGKADL 74
Db 9 PTWPELIGSNMAGLNPDLNDELRELLRCGDFCQVYTFINDQNSYCGSSRYGKADL 74
Qy 75 LKHTAFPGADRFDVAVLYATAKVSPEAFLLKRSREKMDRESNIGYVVSNDSTSR 134
Db 69 FRKVM-LDCEPNDVAFLVATATVTPBEAFLHSLREAMDRESNIGYVVSNDSTSR 127
Qy 135 VAGREYVYVWRCRCRDYEWVDVYGAQLESAPHLRTQOTTTHVEKVENEEKS1HKSSWY 194
Db 128 ELGREGREYVYVWRCRCRDYEWVDVYGAQLESAPHLRTQOTTTHVEKVENEEKS1HKSSWY 165
Qy 195 DCFNINILGASAKDKGSDDDDD--DPKVMQGMWTIYTSSEDPKSPFTKLSARTOLOTK 252
Db 166 ---SLKELKGNKNDGSSSSDEEDDPKPKVMSGMLTIYSDNPKSPFTKLSARTOLOTK 222
Qy 253 LKQMTKYKDELTSTFAGHSLGATLSVVSAPDIVENLTTEIPVTAVVFGCPRVGNKKFQ 312
Db 223 VKSLQHYSSSNPSELVIVGHSGLGATLSVVSAPDIVENGVEVPYTAIVFGSPQVGNKAFN 282
Qy 313 QLPDSYPNLNVLHVRNVIDLIPYVKLMGYVNIIELEIDSRKSTFLKDSKNPSPDMHNL 372
Db 283 ERFNMFPLKVLKVNIDILPHYPGKULGVEYWGTELVIDTRKSPSLKDSKNPSPDMHNL 342
Qy 373 QAILHVVSGMHGKGFVKVYKRSVALVYKSCDFLKEECLVPPAMVVQNKGWVLNKDGE 432
Db 343 QAILHVVAGNMNKKKEEFEMVKSVALVYKSCDFLKEEYVPGSWVWEKKKGVKRRDGE 402
Qy 433 WVLAPPEEDPTPEFD 444
Db 403 WVLADPDEEDVP 414

RESULT 4
US-10-674-540-16
; Sequence 16, Application US/10674540
; Publication No. US20040158891A1
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 1079-10
```

[illegible]

```
Db      66  FNRDPLSRVDV-SNPNIYEITKFIYAMCTVSLPDGFVYKSLSKAAMRSQNMNGFVAVA 124
Qy      129  NDETSRVAGREVVYVWGTCRDYEMVDVLAQLESAPHLRTQOTTHVEKVENEEKSI 188
Db      125  TDEGKEELGRDGVVAMGTTIRMEWVDLDISLVPASEIV----- 165
Qy      189  HKSSWYDFNINLLGSASKGKSGSDDDDDPKVMQGMNTIYSEDEKSPFTKLSARTQ 248
Db      166  -----LPSAA-----NPCVHGMLSVYTSADPGSQYNKESARHQ 200
Qy      249  LQTKLKQMLTKYKDETLSTITFAGHSLGATLSVSAFDIVENLTTE--IPYAVVPGCKV 306
Db      201  VLINEVKRIQDLYKPEETSIITTGSHLGAALATINATDIVSNGYNKSCCPVSAFVPGSPRV 260
Qy      307  GNKKFOOLFDSYPNLVNVAHVNRVIDLIPLYPKLMGVYNIIGIELEIDRSKSTFLKDSKNP 366
Db      261  GNLDFOKAFDSADRLRLRRNSPDVVPKWP--KLGYSDVGTLMIDTIGESPFLYKAPGNP 318
Qy      319  LTHWDMCYMHGVAGAGSSGGFELLVD RDVALVNHEDALRNEFAVPSPMVVYQNKGMV 378
Db      427  LNKGEVVLAPPEED 441
Qy      379  KGKDGWRMLADHEED 393
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## RESULT 7

```
US-10-425-114-72507
; Sequence 72507, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72507
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73170B05_FIL.pep
US-10-425-114-72507
```

```
Query Match      34.6%; Score 824.5; DB 4; Length 410;
Best Local Similarity 39.5%; Pred. No. 9e-70;
Matches 172; Conservative 70; Mismatches 144; Indels 49; Gaps 5;

Qy      9  GLSKGPTMPPELGSNANAGLINPLNDELRELLRCGDFCQYTYTFTINDQSSYCGSSR 68
Db      21  GGNVAKRWEKELNGINWKGVLDPDLDIRRNIINYGELSQATYVGLNRRERSRYAGSGL 80
Qy      69  YGKADLLHKTAPPGADRFVAVLYATAKV-SVPEAFLLKSRSREKMDRESNMIGYVVVS 128
Db      81  FRRRPFRLSRVDV-SNPNIYEITKFIYAMCTVSLPDGFVYKSLSKAAMRSQNMNGFVAVA 139
Qy      129  NDETSRVAGREVVYVWGTCRDYEMVDVLAQLESAPHLRTQOTTHVEKVENEEKSI 188
Db      140  TDEGKEELGRDGVVAMGTTIRMEWVDLDISLVPASEIV----- 180
Qy      189  HKSSWYDFNINLLGSASKGKSGSDDDDDPKVMQGMNTIYSEDEKSPFTKLSARTQ 248
Db      181  -----LPSAA-----NPCVHGMLSVYTSADPGSQYNKESARHQ 215
Qy      249  LQTKLKQMLTKYKDETLSTITFAGHSLGATLSVSAFDIVENLTTE--IPYAVVPGCKV 306
```

```
Db      216  VLINEVKRIQDLYKPEETSIITTGSHLGAALATINATDIVSNGYNKSCCPVSAFVPGSPRV 275
Qy      307  GNKKFOOLFDSYPNLVNVAHVNRVIDLIPLYPKLMGVYNIIGIELEIDRSKSTFLKDSKNP 366
Db      276  GNLDFOKAFDSADRLRLRRNSPDVVPKWP--KLGYSDVGTLMIDTIGESPFLYKAPGNP 333
Qy      367  SDWNLQAILHVVSQMHGVKGEFVKVNRKRSVALYNKSCDFLKEECLVPAPMVVYQNKGMV 426
Db      334  LTHWDMCYMHGVAGAGSSGGFELLVD RDVALVNHEDALRNEFAVPSPMVVYQNKGMV 393
Qy      427  LNKGEVVLAPPEED 441
Db      394  KGKDGWRMLADHEED 408
```

## RESULT 8

```
US-10-437-963-115585
; Sequence 115585, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 115585
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_19168C.1.pep
US-10-437-963-115585
```

```
Query Match      32.5%; Score 775.5; DB 4; Length 422;
Best Local Similarity 37.4%; Pred. No. 4.6e-65;
Matches 172; Conservative 70; Mismatches 135; Indels 83; Gaps 8;

Qy      17  WPELGSNANAGLINPLNDELRELLRCGDFCQYTYTFTINDQSSYCGSSRYGKADLLH 76
Db      13  WREIHGEBDHMKGLDPLDADLRRSVIGYGEIQAQTNDAFIREAWSPPAGACRYSDRPLE 72
Qy      77  KT-APPGADRFVAVLYATAKV-SVPEAFLLKSRSREKMDRESNMIGYVVVNDSTSR 134
Db      73  KQASTQLAIGLYEYTAFFYATAGAGVAPAPMVR-----NRSNMNGYAVATADGVA 125
Qy      135  VAGREVVYVWGTCRDYEMVDVLAQLESAPHLRTQOTTHVEKVENEEKSIHKSSWY 194
Db      126  ALGRDGVVAMGTTIRMEWVDLDISLVPASEIV----- 156
Qy      195  DCPNINLLGSASKGKSGSDDDDDPKVMQGMNTIYSEDEKSPFTKLSARTQ----- 248
Db      157  ----AGVLGAGGRSPA-----PRVHRGWSIYASDPASKYSTLSAREQSHIVDW 202
Qy      249  -----LQTKLKQMLTKYKDETLSTITFAGHSLGATLSVSAFDIVE 288
Db      203  DATSTKPSIYITIGLDYTVYISDEIKRLMDKIKOBEETSIYVGSLSGAATAVATINAAIDVS 262
Qy      289  NLTE---IPYAVVPGCKVGNKKFOOLFDSYPNLVNVAHVNRVIDLIPLYPKLMGVYV 345
Db      263  NGIINHGCAPVTYAVAFACPRVGDGSGFRKLPELGLRLRLRCNSPDVVPKWP--MGYAD 320
Qy      346  IGIELEIDRSKSTFLKDSKNP SDWNLQAILHVVSQMHGVKGEFVKVNRKRSVALYNKSCD 405
```

Db 321 VGVELPVDTRRSPLYKSPGNQAVMHSLECYMHGVAQAQKSGFKEJVDRLVALVNRKVD 380  
Qy 406 FKEECVLPRAWVYQNKGLNDGEMVLAPPEEDPTPE 445  
Db 381 ALKEEYHVPWSVQKDKMVGADGKMLMDYGEBSQ 420

RESULT 9  
US-10-674-540-12  
; Sequence 12, Application US/10674540  
; Publication No. US20040158891A1  
; GENERAL INFORMATION:  
; APPLICANT: John E. THOMPSON et al.  
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE.  
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 10799-10  
; CURRENT APPLICATION NUMBER: US/10/674,540  
; CURRENT FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: 09/597,774  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: 09/250,280  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 09/105,815  
; PRIOR FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatsSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 418  
; TYPE: PRT  
; ORGANISM: Plant  
US-10-674-540-12

Query Match 32.5%; Score 775; DB 4; Length 418;  
Best Local Similarity 37.5%; Pred. No. 5.1e-65;  
Matches 167; Conservative 76; Mismatches 138; Indels 64; Gaps 9;

Qy 17 WPELLGSNANAGLNPINDELRELLRCGDFCQYTYTFINDQSSYCGSSRYKADLLH 76  
Db 23 WRDLSSGNHMKGMQPLDQDLREYLIHGYEMAQGYDTFNFINTESQFAGASISYRKQFPA 82  
Qy 77 KT----APGGADRFVAVLYATAKVSVEPAFLKSRSEKMDRESNMIGYVVVNSDET 132  
Db 83 KVGLEIHP--YTKYKTKFPIATASDIHVPESEFLPISRGSKESNMKGVAVTDDQG 140  
Qy 133 SRVAGREVVYVWGTCDYEVWDLGAQLESAPHLRTQOTTVEKVENEEKSIHKSS 192  
Db 141 TALGRDDIVVWSMGSVQPLEWEDFERGLVNA----- 173  
Qy 193 WYDFENINLGSASKDKGSDDDDDDDPKVMQGMWITYTSEDPKSPPTKLSARTQLOTK 252  
Db 174 -----IKIFG-----BRNDQVQIHQWYSIYMSQDERSPTKTNADQVIRE 215  
Qy 253 LKQIMTKYKDETLSTIFAGHSIGATLSVSAFDIVEN-----LTTEIPTAVVFGCP 304  
Db 216 VGRLEKTKDBEVSITTCGSHLGAALATDSADIDVANGYNRPKSPDKSCVTAFVFPASP 275  
Qy 305 KVGKKEFOQLFDSYPNLVHVRNVTDILPYVYKMGYVNIIGLEIDSRKSTFLDKSK 364  
Db 276 RVGSDPRKLFSGLEDIRLVLRTRMLFDVIPYPP--IGSYEVGDSEFPIDTRKSPYMKSPG 333  
Qy 365 NPSNMHLQALIHVUSGMHGV-KGE-PRVYNKRSVALYNKSCDPLKEECVLPRAWVYQNK 422  
Db 334 NLATFHCEGLYHVAAGTQGTNKADELFLDVERAIGLVNKSVDGLKDCWVPGKRVYLN 393  
Qy 423 KGMVLNKGEMVLAPPEEDPTPEPD 447  
Db 394 KG-AQDDGSWEVLVDHEDNEDLD 417

RESULT 10  
US-10-739-930-6050  
; Sequence 6050, Application US/10739930

; Publication No. US20040216190A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53377)B  
; CURRENT APPLICATION NUMBER: US/10/739,930  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 11088  
; SEQ ID NO 6050  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; OTHER INFORMATION: Clone ID: ARATH-23APR03-C213147\_1.p  
US-10-739-930-6050

Query Match 32.2%; Score 767.5; DB 5; Length 423;  
Best Local Similarity 36.7%; Pred. No. 2.7e-64;  
Matches 162; Conservative 73; Mismatches 151; Indels 55; Gaps 6;

Qy 17 WPELLGSNANAGLNPINDELRELLRCGDFCQYTYTFINDQSSYCGSSRYKADLLH 76  
Db 9 WKVLSSGNHMKGMQPLDQDLREYLIHGYEMSQGYDAFWMDRKSRYAGCYSKRLFA 68  
Qy 77 KTAEPGGADRFVAVLYATAKVSVEPAFLKSRSEKMDRESNMIGYVVVNSDETSRV 135  
Db 69 RTGFLKANPFRYKTKYIATASIKLPISTVSLSDASHVQTNMNGYIATVADQKAM 128  
Qy 136 AGRREVVYVWGTCDYEVWDLGAQLESAPHLRTQOTTVEKVENEEKSIHKSSWYD 195  
Db 129 LGRDDIVVWWSMGSVQPLEWEDFERGLVNA-----IS 160  
Qy 196 CFNINLGSASKDKGSDDDDDDDPKVMQGMWITYTSEDPKSPPTKLSARTQLOTLO 255  
Db 161 VFPT-----DPKDPRIKSGWLDIYASRSRSDYDTSAQEOVQGLKR 205  
Qy 256 LMTKYKDETLSTIFAGHSIGATLSVSAFDIV-----ENLT-----TEIPTAVVFGCPV 306  
Db 206 LLELYKDEEISITFTGSHLGAALVMSVLSAADLVYKKNININLOKKOVPITVFPAGSPRI 265  
Qy 307 GNKKFQQLFDSYPNLVHVRNVTDILPYVYKMGYVNIIGLEIDSRKSTFLDKSKNP 366  
Db 266 GDHNFKNVDSLOGLNLTIRVNPVDAVPHPLL--YSEIGEVLKSTLNSTYLRSLNF 323  
Qy 367 SDWHNLQALIHVUSGMHGVKEEFKVNKRSVALYNKSCDPLKEECVLPRAWVYQNKGV 426  
Db 324 RNYHNLKLYLHGMAGMODTGVFGLKIGRDISLVNKGIDALKEVLPSTWRCIANKGML 383  
Qy 427 LNDGEMVLAPPEEDPTPEPD 447  
Db 384 QMDGTWKLVDVHRRDDDDVD 404

RESULT 11  
US-10-739-930-9783  
; Sequence 9783, Application US/10739930  
; Publication No. US20040216190A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53377)B  
; CURRENT APPLICATION NUMBER: US/10/739,930  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 11088  
; SEQ ID NO 9783  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-C176\_284.p  
US-10-739-930-9783

Query Match 32.1%, Score 766; DB 5; Length 434;  
 Best Local Similarity 36.3%, Pred. No. 3.9e-64;  
 Matches 160; Conservative 76; Mismatches 145; Indels 60; Gaps 5;

QY 11 SKPEPT-----WPELGSNAGLPLNDELRELLRCGDCQVYDTTFINDQSSY 63  
 DB 32 SAPAPVGTVASRRRELLHGENSMKGLDPLDPLRLASIIISYGENVQAAYDAFNTERRSPH 91  
 QY 64 CGSSRYGKADLLHHTAFPGADRPDVAVYLVATAKVSVEAFLLKSRNR--EKMDRESNW 121  
 DB 92 CGACFYGEDLLAGVGVPHGNNTVEYKFIYATSSLPSPSSFLPLPLPSLPVMSRESNW 151  
 QY 122 IGYVVSNDSTSRVAREVYVVRGCRDYEMVVDVLAQLESAPHLRTQOTTHVEKVE 181  
 DB 152 MGYVAVATDEGAALALGRDVIYANRGTYQNMENWVNDLDFAPVAPVLSAASQHLAV- 210  
 QY 182 NEEKSIHKSSWYDCFNINLLGSASKDKGSDDDDDDPYVMQGMWTIYSEDPKSPFT 241  
 DB 211 -----VHHGFLSMYTSNKSSEFT 229  
 QY 242 KLSARLOQLTKQLMTKYKDETSLTFAGHSIGATLSVSAFDIV-----ENLTTEI 294  
 DB 230 KTSARDQVYKVRRLVELYKDEVSITTCGHSLSAVATLNAVLDVSSGINKPGSTKSF 289  
 QY 295 PVTAVVFCGPKYGNKKFOQLFDSYPNLVNLVHRVNIIDLPLYPVKLMGYVNIIGIELIDS 354  
 DB 290 PVTAVVPSPHVCGFRFSAFNSFPDLKALHVNAGDVPMYPP--LGYVDVAVELTIRT 347  
 QY 355 RKSTFLKDSKNPSMHNLOAILHVVSGMHGVKGEFRVVKRSVALVNSCDFLKEBCLVP 414  
 DB 348 IRSPYMRKPATVGTTLHNECYLHGVAEGSAGGFLEVDRIALVNNKADALTDHEHPV 407  
 QY 415 PAMVVVQNKGVNLNKDGEVVL 435  
 DB 408 ACMMVPRHKFMVKGEDGRWTL 428

RESULT 12  
 US-10-437-963-138670  
 ; Sequence 138670, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 138670  
 ; LENGTH: 407  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_40036C.1.pep  
 US-10-437-963-138670

Query Match 31.0%, Score 740.5; DB 4; Length 407;  
 Best Local Similarity 37.5%, Pred. No. 9.9e-62;  
 Matches 163; Conservative 70; Mismatches 139; Indels 63; Gaps 7;  
 QY 17 WPELGSNAGLPLNDELRELLRCGDCQVYDTTFINDQSSYCGSRKGRADLLH 76  
 DB 14 WRELHGDSWGLDPLDPLDRSSILSYGELVQATYDSFNRERRSPHAGACVYGHGDL- 72

QY 77 KTAPEGADRFVDVAVYATAKVSVEAPL---LKSRREKMRRESNMGIVVNSDETS 133  
 DB 73 AAGASNAAGSYATYKFFVATSGLPVEAPFLPLPLPSLPVMSRESNMGVAVATDEGV 132  
 QY 134 RVAGREVVYVVRGCRDYEMVVDVLAQLESAPHLRTQOTTHVEKVENEEKSIHKSSW 193  
 DB 133 AALGRDVIYAMGVTYESLEWVDFPTVPVAP- 166  
 QY 194 YDCFNINLLGSASKDKGSDDDDDDPK--VMQGMWTIYSEDPKSPFTKLSARLOQT 251  
 DB 167 -----VLGAAA-----ANPRALVHRGFLSVYTSNKSOKYKASARDQVLE 208  
 QY 252 KQLQMTKYDETLSTFPAGHSIGATLSVSAFDIEN-----LTTEIPVAVV 300  
 DB 209 EVRLMELYKDEVTSTVVHSHLSGASLATINAVDIYANGANCPASSSSQPCPVTAIV 268  
 QY 301 FCGPKYGNKKFOQLFDSYPNLVNLVHRVNIIDLPLYPVKLMGYVNIIGIELIDSRKSTFL 360  
 DB 269 FASPRVGDGFFKAFASFPLRALHVNAGDVPMYPP--LGYVDVAVKLRISTRSPLY 326  
 QY 361 KDSKNPSMHNLOAILHVVSGMHGVKGEFRVVKRSVALVNSCDFLKEBCLVPVAMVY 420  
 DB 327 RSPCTIETLHNECYLHGVAEGSAGGFLEVDRIALVNNKADALDKKXVPVPRKWS 386  
 QY 421 QNKGMVLNKDGEVVL 435  
 DB 387 KNRCMVXADAGHWAL 401

RESULT 13  
 US-10-437-963-139028  
 ; Sequence 139028, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 139028  
 ; LENGTH: 420  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_40360C.1.pep  
 US-10-437-963-139028

Query Match 30.9%, Score 736; DB 4; Length 420;  
 Best Local Similarity 37.5%, Pred. No. 2.8e-61;  
 Matches 162; Conservative 69; Mismatches 141; Indels 60; Gaps 9;  
 QY 22 GSNAGLPLNDELRELLRCGDCQVYDTTFINDQSSYCGSRKGRADLLHKTAFP 81  
 DB 31 GKDRWDGLDPLDPLDRDIRYGELOATSALICGPAPFPAGASHYAPDAFLRKVR-A 89  
 QY 82 GGAAPDVAVYLVATATVSVEAPFLK--SRSRREKMRRESNMGIVVNSDETSRVVGR 139  
 DB 90 SDPAPVATRVVATSSVRLPDATMPRPAPSAGAMGESHMGYVAVADGVAAKGR 149  
 QY 140 EYVYVVRGCRDYEMVVDVLAQLESAPHLRTQOTTHVEKVENEEKSIHKSSWYDCFNI 199  
 DB 150 DIVVAMGTGRAVEMANDLDTLVPADGV----- 179  
 QY 200 NLIGSASKDKGSDDDDDDPKVMQGMWTIYSEDPKSPFTKLSARLOQLTKQLMTK 259



Db 180 -----GCGPCG-----TQPSVHRGFLSVYTSKSSSPFNKLSABEQVLAETRLRLRA 226  
Qy 260 YKDELTITFAGHSIGATLSVSAFDIYEN-----LTTEIPTAVAVGCPKVGKPKQ 312  
Db 227 YKNCISITITGHSIGALSTLNAIDIVANGYVRGSSRVVPYTAIALASPRVGDQFK 286  
Qy 313 QLEPSYNNLVAVHVRNYIDLIP-LYPVKLMGVNIGLELEIDRSKSTFLKDSKNSPDMMH 371  
Db 287 RAFDSTSNLSLRNAPDVIPTILPSAF--FKOVGELLVDITRRSPYLKNPAGPAQWQH 344  
Qy 372 LQALIHVYSGWHGVKGE---FKVYVNRKSVVALVNRKSCDFLEKECVPPAMVYVONKGMVNL 428  
Db 345 LECTLHVAAGTQGA-GCGAGSLVVDRLDALVYNEVDALRBYGVPPAMVYKKNKGVQN 403  
Qy 429 KQGEVVLAPPEE 440  
Db 404 ASGRWVLQDHBE 415

RESULT 14  
US-10-437-963-153035  
; Sequence 153035, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbaruk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 153035  
; LENGTH: 418  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_53027C.1.pcp  
US-10-437-963-153035

Query Match 30.5%; Score 727; DB 4; Length 418;  
Best Local Similarity 38.2%; Pred. No. 2e-60;  
Matches 175; Conservative 51; Mismatches 158; Indels 74; Gaps 6;

Qy 17 WPELLGSNMAAGLNPINDELRELLRCGDFCQVYDTFINDONSSYCGSSRYKADLLH 76  
Db 5 WREIHGSGHMDGLDPLDVRCLITYGEMIMATYEAFIGEHRSPNAGCMRYHADLFR 64  
Qy 77 K-TAFPGADRPVAVLYATKVSYPEAFLKSRSEKDRSNMIGYVVSNDSTSR 134  
Db 65 RVDSHSGW--YATRIYATANADVAGKVLRLPCBGRATECMWGYVAVATDGA 121  
Qy 135 VAGREYVYVWRGCRDYEWDVLAQOLESAPHLRTQOTTHVEKVENEBKSIHKSSWY 194  
Db 122 ALGRRDVVAWKGQRLAEVADLKLAPASAGIL----- 156  
Qy 195 DCFNINILGSASKDKGSDDDDDPKVMQGMNTIYTSDEPKSPFTLSARTQ----- 248  
Db 157 -----GPGAGDGPDSVHRGYLSVLTSEDQSGELNKGASRMQNKLG 199  
Qy 249 -----LOTKLQMLTKTKDETSTTFAGHSIGATLSVSAFDIYEN----- 289  
Db 200 DPMKQTLKKVLTETARLMDKXDEBETSIYVGHSLGATLATLANADIAANSYNGSSRD 259  
Qy 290 LTTEIPTAVAVGCPKVGKPKQFLPDSYPTLVAVHVRNYIDLIPVVKLMGVNIGIB 349

Db 260 LQACTPVAVVFGSPRTGDRGFDAFRLRLDLRLVNRNBPDRIPHYPP--VGADYGV 317  
Qy 350 LEIDRSKSTFLKDSKNSPDMMHNLQALIHVYSGWHGVKGEFPRVYVNRKSVVALVNRKSCDFLE 409  
Db 318 LLDITRLSPFLRRGSSQSHDLECHLHGVAGWGDHRRGFLVVDRLVALNKPDDCLAD 377  
Qy 410 ECLVPPAMVYVONKGMVNLKQGEVVLAPPEEDPPEFD 447  
Db 378 EYVPVYVNRKSVVALVNRKSCDFLEKECVPPAMVYKKNKGVQN 415

RESULT 15  
US-10-425-115-205760  
; Sequence 205760, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 205760  
; LENGTH: 430  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_119237C.1.pcp  
US-10-425-115-205760

Query Match 30.3%; Score 721.5; DB 4; Length 430;  
Best Local Similarity 36.6%; Pred. No. 7.1e-60;  
Matches 164; Conservative 61; Mismatches 168; Indels 55; Gaps 7;

Qy 3 AEAQPLGSKRPGPTWPELLGSNMAAGLNPINDELRELLRCGDFCQVYDTFINDONSS 62  
Db 23 AAQOSQOSQOSORSMAELSGRDNDGLDPLDGRRAVIRYGLAQTSDAFIGDPS 82  
Qy 63 YCGSSRYGKADLLHKTAFPGADRPVAVLYATKVSYPEAFLKSRSEKDRSNMIGYVVSNDSTSR 122  
Db 83 YAGASRTAPGAFRLRAQAP-DPDAVNTVTRFLYATISSARVFGQFTTRAPPGANSAESNM 141  
Qy 123 GYVVSNDSTSRVAGREYVYVWRGCRDYEWDVLAQOLESAPHLRTQOTTHVEKVEN 182  
Db 142 GYVAVATDAGVARRGRDIYVARRGTGRAVEMANDL----- 177  
Qy 183 BEKSIHKSSWYDFCNINILGSASKDKGSDDDDDPKVMQGMNTIYTSDEPKSPFTK 242  
Db 178 -----DITLVPA-----GVVGPGRGQPPVHRGFLSVYASRNSTSRFNK 218  
Qy 243 LSARTQLTKLQMLTKTKDETSTTFAGHSIGATLSVSAFDIYEN-----LTTEIPT 295  
Db 219 KSACMQLAELIRRLDLYKGENCSITLTGHSLGALSTLTAIDIVANGLVNRGNNDTVP 278  
Qy 296 VTAIVFGCPKVGKPKQFLPDSYPTLVAVHVRNYIDLIPVVKLMGVNIGLELEIDSR 355  
Db 279 VAAIVFGSPRVGDQFGKAFDSDAPGARLLLRNAPDVVPYLPRAAF--YKOVGVALLDTR 337  
Qy 356 KSTFLK-DSTKPSDWNHLQALIHVYSGWHGV--KGEFVYVNRKSVVALVNRKSCDFLEKECL 412  
Db 338 KSPHLKRPGRGPAMHNLCEYLHGVAAGTQGAAGAFSLVDRDVALVNRKVDALSDY 397  
Qy 413 VPPAMVYVONKGMVNLKQGEVVLAPPEE 440  
Db 398 VPPAMVYVONKGMVNLKQGEVVLAPPEE 440

Search completed: December 22, 2005, 19:52:53  
Job time: 114.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 22, 2005, 19:33:42 ; Search time 32.5 Seconds

(without alignments)  
1137.109 Million cell updates/sec

Title: US-10-674-540A-2

Perfect score: 2385

Sequence: 1 MAEAQPLGSKPGPTWPEL.....NKDEWVLAPEEDPPEFD 447

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

1: /cgn2\_6/ptodaca/1/1aa/5 COMB.pep:\*

2: /cgn2\_6/ptodaca/1/1aa/6 COMB.pep:\*

3: /cgn2\_6/ptodaca/1/1aa/H.COMB.pep:\*

4: /cgn2\_6/ptodaca/1/1aa/PTTUS.COMB.pep:\*

5: /cgn2\_6/ptodaca/1/1aa/RE.COMB.pep:\*

6: /cgn2\_6/ptodaca/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2385	100.0	447	2	US-09-610-104C-2
2	2377	99.7	447	2	US-09-610-104C-11
3	1077	45.2	348	2	US-09-610-104C-16
4	775	32.5	418	2	US-09-610-104C-12
5	686.5	28.8	447	2	US-09-610-104C-19
6	684	28.7	448	2	US-09-610-104C-14
7	580.5	24.3	195	2	US-09-610-104C-17
8	576.5	24.2	401	2	US-09-610-104C-13
9	129.5	5.4	281	2	US-08-952-445-28
10	129.5	5.4	281	2	US-09-981-430-28
11	122.5	5.1	291	1	US-08-434-255-13
12	122.5	5.1	291	1	US-08-459-967-13
13	122.5	5.1	291	1	US-08-460-327-13
14	122.5	5.1	291	1	US-08-459-871-13
15	122.5	5.1	291	1	US-08-244-686-4
16	122.5	5.1	291	1	US-08-784-651-16
17	122.5	5.1	291	1	US-08-921-426-10
18	122.5	5.1	291	1	US-08-479-2750-2
19	122.5	5.1	291	1	US-08-488-2718-2
20	122.5	5.1	291	1	US-08-140-008A-2
21	122.5	5.1	291	1	US-08-701-339-2
22	122.5	5.1	291	1	US-08-816-915-10
23	122.5	5.1	291	2	US-09-024-532-6
24	122.5	5.1	291	2	US-09-007-288E-16
25	122.5	5.1	291	2	US-09-705-185-6
26	122.5	5.1	291	2	US-09-500-135C-227
27	122.5	5.1	291	2	US-09-768-080-227

28	122.5	5.1	291	2	US-09-677-822A-227	Sequence 227, App
29	122.5	5.1	291	4	PCT-US95-07743-10	Sequence 10, Appl
30	122.5	5.1	384	2	US-09-295-744A-14	Sequence 14, Appl
31	119.5	5.0	294	2	US-09-007-288E-142	Sequence 142, App
32	119.5	5.0	294	2	US-09-007-288E-143	Sequence 143, App
33	118.5	5.0	297	2	US-09-402-664A-9	Sequence 9, Appl
34	118.5	5.0	297	2	US-10-040-394-9	Sequence 9, Appl
35	117	4.9	130	2	US-09-434-840-33	Sequence 33, Appl
36	116.5	4.9	279	2	US-10-369-800-2	Sequence 2, Appl
37	115.5	4.8	297	1	US-08-859-106A-2	Sequence 2, Appl
38	110.5	4.6	130	2	US-09-434-840-32	Sequence 32, Appl
39	110.5	4.6	269	2	US-09-630-250B-19	Sequence 19, Appl
40	110.5	4.6	269	2	US-09-937-919-1	Sequence 1, Appl
41	110.5	4.6	270	2	US-08-362-525-8	Sequence 8, Appl
42	110.5	4.6	289	2	US-09-007-288E-145	Sequence 145, App
43	110.5	4.6	378	2	US-09-395-017B-1	Sequence 1, Appl
44	110.5	4.6	391	2	US-09-395-017B-2	Sequence 2, Appl
45	108	4.5	197	2	US-08-952-445-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1					
US-09-610-104C-2					
Sequence 2, Application US/09610104C					
Patent No. 6774284					
GENERAL INFORMATION:					
APPLICANT: John E. THOMPSON et al.					
TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,					
TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN					
PLANTS					
FILE REFERENCE: 10799-10					
CURRENT APPLICATION NUMBER: US/09/610,104C					
CURRENT FILING DATE: 2000-07-05					
PRIOR APPLICATION NUMBER: 09/597,774					
PRIOR FILING DATE: 2000-06-09					
PRIOR APPLICATION NUMBER: 09/250,280					
PRIOR FILING DATE: 1999-02-16					
PRIOR APPLICATION NUMBER: 09/105,815					
PRIOR FILING DATE: 1998-06-26					
NUMBER OF SEQ ID NOS: 21					
SOFTWARE: FastSeq for Windows Version 4.0					
SEQ ID NO 2					
LENGTH: 447					
TYPE: PRT					
ORGANISM: Plant					
US-09-610-104C-2					
Query Match					
Best Local Similarity 100.0%; Pred. No. 8.9e-248; Length 447;					
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MAEAQPLGSKPGPTWPELGSNAAGLNPINDELRELLRCGDFCOVYDTFINDN	60		
Db	1	MAEAQPLGSKPGPTWPELGSNAAGLNPINDELRELLRCGDFCOVYDTFINDN	60		
Qy	61	SSYCGSSRYGKADILHTTAPPGADRPDYVAYATKAVSYPEAFLLKSRREWDSESN	120		
Db	61	SSYCGSSRYGKADILHTTAPPGADRPDYVAYATKAVSYPEAFLLKSRREWDSESN	120		
Qy	121	WIGVVVSNDETSTVARRREVVYVWRTGCRDYENVDLGAOLSAHFLTRQOTTHYEKV	180		
Db	121	WIGVVVSNDETSTVARRREVVYVWRTGCRDYENVDLGAOLSAHFLTRQOTTHYEKV	180		
Qy	181	ENEKKSIRHSSWYDCFNILGASAKDKGSDDDDDPKVQGMWITYTSDPKSPF	240		
Db	181	ENEKKSIRHSSWYDCFNILGASAKDKGSDDDDDPKVQGMWITYTSDPKSPF	240		
Qy	241	TKLSARFQLOTKLKQMTKTKKDETLSTTPAGHSIGATLSVVSAPFDYENLTTEIPYNAV	300		
Db	241	TKLSARFQLOTKLKQMTKTKKDETLSTTPAGHSIGATLSVVSAPFDYENLTTEIPYNAV	300		

```
Qy 301 FGCPCVGNKKFQOQLFDSYPNINLVHVRNVIDLIPYVKMGVYNGIELEIDSRKSTFL 360
|
Db 301 FGCPCVGNKKFQOQLFDSYPNINLVHVRNVIDLIPYVKMGVYNGIELEIDSRKSTFL 360
Qy 361 KDSKNPBDWMHNLQAILHVSGMHGKGFVKVKNRSVALVNSKCDPLKECLVPPAMVV 420
|
Db 361 KDSKNPBDWMHNLQAILHVSGMHGKGFVKVKNRSVALVNSKCDPLKECLVPPAMVV 420
Qy 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447
|
Db 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447
```

```
RESULT 2
US-09-610-104C-11
; Sequence 11, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Plant
; US-09-610-104C-11
```

```
Query Match 99.7%; Score 2377; DB 2; Length 447;
Beet Local Similarity 99.8%; Pred. No. 6.4e-247;
Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MAEAOPGLGSKPGTPELIGSNMAGLNPINDELLELLRCDFQCVTYDFEINDON 60
|
Db 1 MAEAOPGLGSKPGTPELIGSNMAGLNPINDELLELLRCDFQCVTYDFEINDON 60
Qy 61 SSYCGSSRYGKADLLHKTAFPGADRFDVVAIYATKAVSPEAFLLKSRSREKMDRESN 120
|
Db 61 SSYCGSSRYGKADLLHKTAFPGADRFDVVAIYATKAVSPEAFLLKSRSREKMDRESN 120
Qy 121 WIGYVVNSDETSTRVAGREYVYVWRCRCRDYEWVDVGAQLESNAHPLRTQOTTHVEKV 180
|
Db 121 WIGYVVNSDETSTRVAGREYVYVWRCRCRDYEWVDVGAQLESNAHPLRTQOTTHVEKV 180
Qy 181 ENBEKKSJHKSQWDCFNINILGSASKDGKSDDDDDDDPKVMGMMTITSEDPKSPF 240
|
Db 181 ENBEKKSJHKSQWDCFNINILGSASKDGKSDDDDDDDPKVMGMMTITSEDPKSPF 240
Qy 241 TKLSARQLOTLKQLMTKYDETLSTPAGHSLGATLSVSAFDIVENLTTEIPVNAV 300
|
Db 241 TKLSARQLOTLKQLMTKYDETLSTPAGHSLGATLSVSAFDIVENLTTEIPVNAV 300
Qy 301 FGCPCVGNKKFQOQLFDSYPNINLVHVRNVIDLIPYVKMGVYNGIELEIDSRKSTFL 360
|
Db 301 FGCPCVGNKKFQOQLFDSYPNINLVHVRNVIDLIPYVKMGVYNGIELEIDSRKSTFL 360
Qy 361 KDSKNPBDWMHNLQAILHVSGMHGKGFVKVKNRSVALVNSKCDPLKECLVPPAMVV 420
|
Db 361 KDSKNPBDWMHNLQAILHVSGMHGKGFVKVKNRSVALVNSKCDPLKECLVPPAMVV 420
Qy 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447
|
Db 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447
```

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Db 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447
|
RESULT 3
US-09-610-104C-16
; Sequence 16, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Plant
; US-09-610-104C-16
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Query Match 45.2%; Score 1077; DB 2; Length 348;

Beet Local Similarity 55.2%; Pred. No. 5.1e-107;

Matches 201; Conservative 63; Mismatches 74; Indels 26; Gaps 3;

```
Qy 84 ADREPVAVIYATKAVSPEAFLLKSRSREKMDRESNIGYVVNSDETSTRVAGREYV 143
|
Db 10 ASDYEVNPLIYATKAVSPEAFLLKSRSREKMDRESNIGYVVNSDETSTRVAGREYV 143
Qy 144 VWRGTCRDYEWVDVGAQLESNAHPLRTQOTTHVEKVENBEKKSJHKSQWDCFNINILG 203
|
Db 70 ALRGTSNTEYEVNVLGARPSTADPLHGP-----EQDGGGVVGTTFD----- 113
Qy 204 SASDKKGGSDDDDDPKVMGMMTITSEDPKSPFKLSARQLOTLKQLMTKYKDE 263
|
Db 114 -----SDSEBECCKWLGWLTITYSNHPKSKTKLSRQLOLAKIKELLYKDE 164
Qy 264 TLSTPAGHSLGATLSVSAFDIVENLTTEIPVNAVFGCPKVGKKNKFOQLFDSYPNIN 322
|
Db 165 KPSTIVLTGHSIGPTBEAVLAATIDENSSDDVPYTAIVFGCPYGNKEFRDEWVSHKTLK 224
Qy 323 VLAHVRNVIDLIPYVKMGVYNGIELEIDSRKSTFLKDSKNPBDWMHNLQAILHVSGW 382
|
Db 225 ILHVRNVIDLIPYVKMGVYNGIELEIDSRKSTFLKDSKNPBDWMHNLQAILHVSGW 284
Qy 383 HGKGFVKVKNRSVALVNSKCDPLKECLVPPAMVVQNKGWVLNKDGEWVLAPPEED 442
|
Db 285 NGKGFVKVKNRSVALVNSKCDPLKECLVPPAMVVQNKGWVLNKDGEWVLAPPEED 344
Qy 443 TPEF 446
|
Db 345 VPEF 348
|
RESULT 4
US-09-610-104C-12
; Sequence 12, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
```



```

Dh 22 TWKTKIQGSDDMWGLMDPMDPIKRSBILIRYGENAQAACYDAFDDPASKYTCGTSRFTLREFF 81
Qy 76 HKTAFFPGADR-FDVVAALYATAKVSVBPAPFLKRSRKMDRESNMIGYVVVSDETS 134
Dh 82 DSL---GNIDSGYEVARLYATSNINLPR-FPSKSMKSVKMGNAWVGVAVSDETS 137
Qy 135 -VAGREVVYVWRGTCRDYEWVDVIGAQESAHPLIRTOQTHVEKEVENEKSKIHKSM 193
Dh 138 NRIIGRDIAMRGVTVTKLEWIAIDKDYKPV-----TENKIR----- 175
Qy 194 YDCFRINILGSAKSKGKSGDDDDDDPRVMOGMWITYSEDKPSFTLSARTOQTKL 253
Dh 176 --C-----PDAVVGESGFIDLTYDKOTCKCFARPSAEQILTEV 213
Qy 254 KOLMTKYKDE---TLSTIPAGHSIGTISVNSAFDIVE---NLTTB---IPYTAVV-FGC 303
Dh 214 KRLVHEHDDDDSDSITVTGSHSGALAILSNAYDLAEKRLKRSKGKXVIPYAVLTYGG 273
Qy 304 PRVGNKKEFOQLFDSYPNLNLVLRNVYIDLPLYPVKLMG-----YVNI 346
Dh 274 PRGVNVRFRERNEEL-GVKVMRVVVNVHDVVPSPGFLMESRPHALMKIAEGLPMCYSHV 332
Qy 347 GIELEIDSKSTFFLKDSKNPSDMNIOALILHVVSCHNGYKGE-FKVVNKRSAVLVVKSCD 405
Dh 333 GSELIDLHONSPEFLKPSVDVSTAHNLEAMILHLLDGYHG-KGERFVLVSGRDHALVVKASD 391
Qy 406 FLKEECIVPRAMVVVQNKGMVLNKDEGEMLA 436
Dh 392 FLKEHLQIPEFRQDANKGMVNSBSRWIQA 422

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```

RESULT 7
US-09-610-104C-17
; Sequence 17, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LTPASE.
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Plant
US-09-610-104C-17

```

	Query Match	24.3%	Score 580.5	DB 2	Length 195
	Best Local Similarity	53.4%	Pred. No. 6.1e-54		
	Matches 119	Conservative 31	Mismatches 44	Indels 29	Gaps 4
Qy	151	DYEWVDVLAQLESAPHLIRTOQTTHVEKEVENEKKSIIHKSWSYDCFNINLLGASAKDKG	210		
	1	DYEWVDVLAQARDSADSL-	-----HPSLQK-----GIN-----NKN	32	
Db	211	KGSDDDDDDPKVMQGMWTTIYSEDPKSPPTKLSAATQLOTKYKQMTKYKDETLSTFA	270		
	:::	:::	:::	:::	:::
Qy	33	DEDEDEDEBEIKVMQGMWTKIYVSSNPKSFFTRLSAREQLOAKTEKIRNEKXENLSITFT	92		
Db	271	GHSIDATLSVSAFPIVFN-LTTEIPVTVAVEGCPKRVGNKKPQQLPDSYNNLVHLVRYNV	329		
Qy	93	GHSIDATLSVSAFPIVFN-LTTEIPVTVAVEGCPKRVGNKKPQQLPDSYNNLVHLVRYNV	329		
Db	152	GHSIDATLSVSAFPIVFN-LTTEIPVTVAVEGCPKRVGNKKPQQLPDSYNNLVHLVRYNV	329		

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QY      330 IDLIPLPYVKLMGVNIGIELEIDSRKSTFLKDSKNPSDWHNL 372
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      153 IDLITLPSALFGVNSGIELVIDSRKSPSLKDSKMDGMDWHNL 195
Db
```

```

      RESULT 8
      US-09-610-104C-13
      ; Sequence 13, Application US/09610104C
      ; Patent No. 6774284
      ; GENERAL INFORMATION:
      ; APPLICANT: John E. THOMPSON et al.
      ; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
      ; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESCENCE IN
      ; TITLE OF INVENTION: PLANTS
      ; FILE REFERENCE: 10799-10
      ; CURRENT APPLICATION NUMBER: US/09/610,104C
      ; CURRENT FILING DATE: 2000-07-05
      ; PRIOR APPLICATION NUMBER: 09/597,774
      ; PRIOR FILING DATE: 2000-06-09
      ; PRIOR APPLICATION NUMBER: 09/250,280
      ; PRIOR FILING DATE: 1999-02-16
      ; PRIOR APPLICATION NUMBER: 09/105,815
      ; PRIOR FILING DATE: 1998-06-26
      ; NUMBER OF SEQ ID NOS: 21
      ; SOFTWARE: FastSeq for Windows Version 4.0
      ; SEQ ID NO 13
      ; LENGTH: 401
      ; TYPE: prt
      ; ORGANISM: Plant
      ; US-09-610-104C-13

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Query Match	24.2%	Score 576.5;	DB 2;	Length 401;
Best Local Similarity	10.8%	Pred. No. 5.5e-53;		
Match 138;	Conservative	79;	Mismatches 166;	Indels 63; Gaps 8

  

QY	9	GLSKRGPWPELLGSNAWAGLNLPLNDELRLRELLRCGDGFCQVYDTFTINDNSSYCGSSR	68
DB	3	GIAC---RWKVLVSGSDWEGGLEPLDSDLTRRYLLHYGTWVSPATDSSFINEAASKVGLPR	59
QY	69	YGGADLHKTA-F-EGGADRPDVAVLYLTATKAVSP-EAFLLKSKSRREKMDSENNIGYVV	126
DB	60	YARRLLANCGLVKGNPKPEVETKYFYAPSTPLPEDESYNVRATPADVLKESMNGYVA	119
QY	127	VSNDETSVAGRREYVVVWVRGTCRDYEWADVLAGQLBSAHPDLRTQOQTHYEKENEKK	186
DB	120	VATDEGKALARRDRLIYWRGTIIKSENNELTFWYVA-PLPFGQ-----	164
QY	187	SIHKSWSYDCFNILLGSASKDGKSGDDDDDDPKVMQGMITYTSEDSPKSPFTKLSAR	246
DB	165	-----NSDPLVHKGWYDMVYTTINQSOQLNEKSR	193
QY	247	TOLQTKLQMLTKYKDETLSTTFAGHSIGATLVSAADYE---NLTELRYAVAVSGC	303
DB	194	DQIREVAVRLVELYXDEDISTITVGHSGSSMATLNADVLANPINNKNILVTAFLVAS	253
QY	304	PKVGGKKKQOOLFDSYXPNLVAVENVLDLILPLVP-----KLMGYVNIIGIELEIDSR	355
DB	254	PKVGEENKKNVINSQNLRALRISGVNDIVTAVRPFQWKECDNMTALIVGDVGVGLVIDSK	313
QY	356	KSTFLKDSKNPSDWMNTLQAILIHVVSQMTGVGGEFRVNVKKSVALYNKSCDFLKECCLVP	415
DB	314	KSHYLKRPFPNLSTHDLMLYMHAILDYGXSGSGGFERODFDLAKVKNKGDYLKAEYPIPI	373
QY	416	AMVVVQNKGMVLNKGEMVLARPEEDPT	443
DB	374	GMFNIXDKGM-QQDDGNYILLDHEVDKT	400

  

RESULT 9
US-08-952-445-28
; Sequence 28, Application US/08952445
; Patent No. 6368833

GENERAL INFORMATION:  
APPLICANT: Genencor International, Inc.  
TITLE OF INVENTION: ESTERASE ENZYMES, DNA ENCODING  
TITLE OF INVENTION: ESTERASE ENZYMES AND VECTORS AND HOST CELLS INCORPORATING SAME  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genencor International, Inc.  
STREET: 925 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1013  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/952,445  
FILING DATE: 18-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/722,713  
FILING DATE: 30-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Stone, Christopher L.  
REGISTRATION NUMBER: 35,696  
REFERENCE/DOCKET NUMBER: GC362-2-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-846-7555  
TELEFAX: 650-845-6504  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-952-445-28

Query Match 5.4%; Score 129.5; DB 2; Length 281;  
Best Local Similarity 24.6%; Pred. No. 4.4e-05;  
Matches 64; Conservative 38; Mismatches 81; Indels 77; Gaps 12;

157 VLAQLESAPHLRTQOTTHVEKEN-EKKSIHKSWMYCFNIN----- 200  
9 VLAVVVAGHALAASSTGISEDLSRLVENATISQAAYADLCNIPSTTIKGEKTYNSQTD 68  
201 -----LIGSASKD-----KKGSGDDDDDDPKVMQGMWITYTSEDPKSPFTKL----- 243  
69 INGMILRDDSKEIITVFRGTGSDTNQLD-----TNYT-----LTPDITLPQNGCE 116  
244 -----SARTQLOTKLKQMTKYKDETLSTTFAGHSLGATLSVVSAPDIVENLTTE 293  
117 VHGGYIIGWVSVDQVESLVKQOVQYPDYALTVT--GHSIGASIALTAOL---SATY 171  
294 IPTAVAVGCPKGNKKFQOLFDSYPN-----LNVLHVRNVIDLPLVPVKLMGY 343  
172 DNIILTYFGESRGN---QAFASYMDAFQASSPDTTQYFRVTHANDGILNLPVEQGY 227

344 VNIGIEL-EID--SRKSTFL 360  
228 AHGVEYWSVDPPYSAQNTFV 247

RESULT 10  
US-09-981-430-28  
Sequence 28, Application US/09981430  
Patent No. 6828136  
GENERAL INFORMATION:  
APPLICANT: Genencor International, Inc.  
TITLE OF INVENTION: ESTERASE ENZYMES, DNA ENCODING  
ESTERASE ENZYMES AND VECTORS AND HOST CELLS INCORPORATING S  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genencor International, Inc.  
STREET: 925 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1013  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/981,430  
FILING DATE: 15-Oct-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/952,445  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Stone, Christopher L.  
REGISTRATION NUMBER: 35,696  
REFERENCE/DOCKET NUMBER: GC362-2-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-846-7555  
TELEFAX: 650-845-6504  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
US-09-981-430-28

Query Match 5.4%; Score 129.5; DB 2; Length 281;  
Best Local Similarity 24.6%; Pred. No. 4.4e-05;  
Matches 64; Conservative 38; Mismatches 81; Indels 77; Gaps 12;

157 VLAQLESAPHLRTQOTTHVEKEN-EKKSIHKSWMYCFNIN----- 200  
9 VLAVVVAGHALAASSTGISEDLSRLVENATISQAAYADLCNIPSTTIKGEKTYNSQTD 68  
201 -----LIGSASKD-----KKGSGDDDDDDPKVMQGMWITYTSEDPKSPFTKL----- 243  
69 INGMILRDDSKEIITVFRGTGSDTNQLD-----TNYT-----LTPDITLPQNGCE 116  
244 -----SARTQLOTKLKQMTKYKDETLSTTFAGHSLGATLSVVSAPDIVENLTTE 293  
117 VHGGYIIGWVSVDQVESLVKQOVQYPDYALTVT--GHSIGASIALTAOL---SATY 171  
294 IPTAVAVGCPKGNKKFQOLFDSYPN-----LNVLHVRNVIDLPLVPVKLMGY 343  
172 DNIILTYFGESRGN---QAFASYMDAFQASSPDTTQYFRVTHANDGILNLPVEQGY 227

344 VNIGIEL-EID--SRKSTFL 360  
228 AHGVEYWSVDPPYSAQNTFV 247

RESULT 11  
US-08-434-255-13  
Sequence 13, Application US/08434255  
Patent No. 5621089  
GENERAL INFORMATION:  
APPLICANT: Sloma, Alan P.  
APPLICANT: Outtrup, Heile  
APPLICANT: Dammann, Claus  
APPLICANT: Aaslyng, Dorrit  
TITLE OF INVENTION: ALKALINE PROTEASE  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5621089 No. 5621089isk of No. 5621089th America, Inc.  
STREET: 405 Lexington Avenue, 64th Floor  
CITY: New York

STATE: New York  
COUNTRY: USA  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/434,255  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Agilis Dr., Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3764,400-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 291 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-434-255-13

Query Match 5.1%; Score 122.5; DB 1; Length 291;  
Best Local Similarity 17.7%; Pred. No. 0.00027;  
Matches 59; Conservative 55; Mismatches 120; Indels 99; Gaps 12;

QY 24 NAMAGLPLNDELRELLRCGDFCQVYDTPFINDQSSYCGSSRYGKADLLHKTAFPGG 83  
DB 11 SAMTALSPIRREVSQLFN-----QFNLFQAGYAAACGKNDA-----PAG 53  
QY 84 ADFPDVAAYLYATKAVSPEAFLLKRSREKMDRESNMIGYV--VSNDETSRVAGREV 141  
DB 54 T---NITCTGNACPEVEKADATFL-----YSFEDSGVGDTGFLADNTNKL-----I 98  
QY 142 YVWAGTCRDYEWVDVLAQLESAPLRLRQOQTHVEKVENEEKSIHKSWSYDGFNINL 201  
DB 99 VLSFRGSRISLNMIGNLN-----FDLKEIND 124  
QY 202 LGSASKDKGSGDDDDDDPKVMQGMITYTSEDDPKSPFTKLARTOLQTKLQMLTKYK 261  
DB 125 ICSGC---RGHDG-----FTSSMRSVADT-----LRQVEDAVAREHP 158  
QY 262 DETLSITPAGSLGATLSVSAFDIVENLTTEIPVTAVVFGCPKVGKKFQQLFDSYPNL 321  
DB 159 D--YRVVFTGHSIGALATVAGADLRGN---GYDIDVFSYGAPRVGNRAFAEFLTVQTGG 213  
QY 322 NVLHVRNVIDLPIYPVKLMGYVNIIGIELEIDS 354  
DB 214 TLVRIHTNDIVPRLPRREFGSHSSPEYWIKS 246

RESULT 12

US-08-459-967-13

Sequence 13, Application US/08459967

Patent No. 5622841

GENERAL INFORMATION:

APPLICANT: Sloma, Alan P.

APPLICANT: Outtrup, Helge

APPLICANT: Dammann, Claus

APPLICANT: Aaslyng, Dorrit

TITLE OF INVENTION: ALKALINE PROTEASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5622841 of No. 5622841th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,967  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/434,255  
FILING DATE: 03-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Agilis Dr., Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3764,400-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 291 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-459-967-13

Query Match 5.1%; Score 122.5; DB 1; Length 291;  
Best Local Similarity 17.7%; Pred. No. 0.00027;  
Matches 59; Conservative 55; Mismatches 120; Indels 99; Gaps 12;

QY 24 NAMAGLPLNDELRELLRCGDFCQVYDTPFINDQSSYCGSSRYGKADLLHKTAFPGG 83  
DB 11 SAMTALSPIRREVSQLFN-----QFNLFQAGYAAACGKNDA-----PAG 53  
QY 84 ADFPDVAAYLYATKAVSPEAFLLKRSREKMDRESNMIGYV--VSNDETSRVAGREV 141  
DB 54 T---NITCTGNACPEVEKADATFL-----YSFEDSGVGDTGFLADNTNKL-----I 98  
QY 142 YVWAGTCRDYEWVDVLAQLESAPLRLRQOQTHVEKVENEEKSIHKSWSYDGFNINL 201  
DB 99 VLSFRGSRISLNMIGNLN-----FDLKEIND 124  
QY 202 LGSASKDKGSGDDDDDDPKVMQGMITYTSEDDPKSPFTKLARTOLQTKLQMLTKYK 261  
DB 125 ICSGC---RGHDG-----FTSSMRSVADT-----LRQVEDAVAREHP 158  
QY 262 DETLSITPAGSLGATLSVSAFDIVENLTTEIPVTAVVFGCPKVGKKFQQLFDSYPNL 321  
DB 159 D--YRVVFTGHSIGALATVAGADLRGN---GYDIDVFSYGAPRVGNRAFAEFLTVQTGG 213  
QY 322 NVLHVRNVIDLPIYPVKLMGYVNIIGIELEIDS 354  
DB 214 TLVRIHTNDIVPRLPRREFGSHSSPEYWIKS 246

RESULT 13

US-08-460-327-13

Sequence 13, Application US/08460327

Patent No. 5622850

GENERAL INFORMATION:

APPLICANT: Sloma, Alan P.

APPLICANT: Outtrup, Helge

APPLICANT: Dammann, Claus

APPLICANT: Aaslyng, Dorrit

TITLE OF INVENTION: ALKALINE PROTEASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5622850 of No. 5622850th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York



COUNTRY: USA  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,327  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/434,255  
FILING DATE: 03-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Agilis Dr., Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3764,400-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 291 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-460-327-13

Query Match 5.1%; Score 122.5; DB 1; Length 291;  
Best Local Similarity 17.7%; Pred. No. 0.00027;

Matches 59; Conservative 55; Mismatches 120; Indels 99; Gaps 12;

QY 24 NAWAGLPLNDELRLRCGDFCQVYDTFTINDNSSYCGSRYGKADLHKTAPGG 83  
DB 11 SAMTALASPIRREVSDLFN-----QFNLFAGYSAAYCGKNDA-----PAG 53  
QY 84 ADRPDVAVIYATKAVPEAFLLKSRREKMDRESNIGVY--VNDSTSRVAGREV 141  
DB 54 T--NITCTGNACPEVEKADATFL-----YSPEDSGVDGVTGFLADNTNKL-----I 98  
QY 142 YVWRGTCRDYEWVDVGAQLSAPLRTQOTTHVEKVENEEKSIHKSWMYDCEFNIL 201  
DB 99 VLSFRGSRISLNNIGNLN-----FTSSWRSVADT-----LRQVEDAVREHP 124  
QY 202 LGSASDKGSGSDDDDDDPKMGWMTIYTSBDPKSPFTKLSARTQLQTKLQMLTKYK 261  
DB 125 ICSGCC-----RGHDG-----FTSSWRSVADT-----LRQVEDAVREHP 158  
QY 262 DETLSTFAGHSIGATLSVVSAPDIYENLTTEIPVTAIVFGCPKVGKKFQQLFDSYFNL 321  
DB 159 D--YRVVFTGHSIGGALATVAGADLRGN--GYDIDVFSYGAPRVGRFAEFLLVQTGG 213  
QY 322 NVLHVRNVLDILPLYPVKLMGVNIGIELEIDS 354  
DB 214 TVLRITHNDIVPLRPREFGYSHSPETWIKS 246

RESULT 14  
US-08-459-871-13  
Sequence 13, Application US/08459871  
Patent No. 5650326  
GENERAL INFORMATION:  
APPLICANT: Sloma, Alan P.  
APPLICANT: Outtrup, Heile  
APPLICANT: Dammann, Claus  
APPLICANT: Aaslyng, Dorrit  
TITLE OF INVENTION: ALKALINE PROTEASE  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: No. 5650326 No. 5650326disk of No. 5650326th America, Inc.  
STREET: 405 Lexington Avenue, 64th Floor  
CITY: New York

STATE: New York  
COUNTRY: USA  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,871  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/434,255  
FILING DATE: 03-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Agilis Dr., Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3764,400-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 291 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-459-871-13

Query Match 5.1%; Score 122.5; DB 1; Length 291;  
Best Local Similarity 17.7%; Pred. No. 0.00027;

Matches 59; Conservative 55; Mismatches 120; Indels 99; Gaps 12;

QY 24 NAWAGLPLNDELRLRCGDFCQVYDTFTINDNSSYCGSRYGKADLHKTAPGG 83  
DB 11 SAMTALASPIRREVSDLFN-----QFNLFAGYSAAYCGKNDA-----PAG 53  
QY 84 ADRPDVAVIYATKAVPEAFLLKSRREKMDRESNIGVY--VNDSTSRVAGREV 141  
DB 54 T--NITCTGNACPEVEKADATFL-----YSPEDSGVDGVTGFLADNTNKL-----I 98  
QY 142 YVWRGTCRDYEWVDVGAQLSAPLRTQOTTHVEKVENEEKSIHKSWMYDCEFNIL 201  
DB 99 VLSFRGSRISLNNIGNLN-----FTSSWRSVADT-----LRQVEDAVREHP 124  
QY 202 LGSASDKGSGSDDDDDDPKMGWMTIYTSBDPKSPFTKLSARTQLQTKLQMLTKYK 261  
DB 125 ICSGCC-----RGHDG-----FTSSWRSVADT-----LRQVEDAVREHP 158  
QY 262 DETLSTFAGHSIGATLSVVSAPDIYENLTTEIPVTAIVFGCPKVGKKFQQLFDSYFNL 321  
DB 159 D--YRVVFTGHSIGGALATVAGADLRGN--GYDIDVFSYGAPRVGRFAEFLLVQTGG 213  
QY 322 NVLHVRNVLDILPLYPVKLMGVNIGIELEIDS 354  
DB 214 TVLRITHNDIVPLRPREFGYSHSPETWIKS 246

RESULT 15  
US-08-244-686-4  
Sequence 4, Application US/08244686  
Patent No. 570358  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Process for the production of a protein  
TITLE OF INVENTION: using endoxylanase II (exIIa) expression signals  
NUMBER OF SEQUENCES: 12  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

;  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/244,686  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 291 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-244-686-4

Query Match 5.1%; Score 122.5; DB 1; Length 291;  
Best Local Similarity 17.7%; Pred. No. 0.00027;  
Matches 59; Conservative 55; Mismatches 120; Indels 99; Gaps 12;

QY 24 NAMAGLNPENDELRLRCGDPQVYTDTFINDQNSYCGSSRYGKADLLHKTAFPG 83  
Db 11 SAWTALASPIRREVVSQDLFN-----QFNLFAQYSAAYCGKNDA-----PAG 53  
QY 84 ADRPDVVAYLYATAKVSVEAFLLKSRSEKMDRESNMIGYV--VSNDTSRVAGRREV 141  
Db 54 T--NITCTGNACPEVEKADATFL-----YSFEDSGVDVTGFLADNTNKL-----I 98  
QY 142 YVVRGTCRDYEWVDVGAQLSAHPLRTQOTTHVEKEVNEBKKSIIHKSMYDCFNINL 201  
Db 99 VLSFRGSRSIENWIGNLN-----FDLKEIND 124  
QY 202 LGSASKDKGSGDDDDDDPKVMGMMTIYTSDEPKSPFTKLSARTOLQTKLQOLMTKYK 261  
Db 125 ICSGC---RGHDG-----FTSGWRSVADT-----LRKVEDAVREHP 158  
QY 262 DETLSITPAGSLGATLSVSAFDIVENLTTEIPVTAVVFGCPKVGNKKFOOLFDSYPNL 321  
Db 159 D--YRVVFTGHSLGALATVAGADLRGN---GYDIDVFSYGAFRVGNRAFAEFLTVQTGG 213  
QY 322 NVLHVRNVIDLPLYPVKLMGYVNIIGLEIDS 354  
Db 214 TLVYRITHNDIVPRLPREFGYSHSSPEYWIKS 246

Search completed: December 22, 2005, 19:49:01  
Job time : 34.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 22, 2005, 19:33:07 ; Search time 131.5 Seconds  
(without alignments)  
1493.554 Million cell updates/sec

Title: US-10-674-540A-2  
Perfect score: 2385  
Sequence: 1 MAABQAQPLGLSKPGPTWPEL.....NKDGEWTLAPPEEDPTPEFD 447

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*
- 9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2385	100.0	447	3	AAV97298 Senescenc
2	2377	99.7	447	3	AAV97304 Senescenc
3	2377	99.7	447	5	AAU11997 Carnation
4	1311.5	55.0	412	3	AAAG29751 Arabidops
5	1311.5	55.0	412	5	ABB92084 Arabidops
6	1311.5	55.0	412	8	ADU20619 Arabidops
7	1311.5	55.0	412	8	ADU20462 A. thalia
8	1311.5	55.0	418	3	AAAG29750 Arabidops
9	1082	45.4	343	3	AAAG29752 Arabidops
10	1077	45.2	348	5	AAV97308 Carnation
11	1077	44.2	348	5	AAU12003 Carnation
12	1054	44.2	510	7	ABM86048 Rice abio
13	824.5	34.6	410	8	ADY24723 Plant ful
14	789.5	33.1	419	5	ABM92980 Herbicida
15	775	32.5	418	3	AAV97305 Senescenc
16	770.5	32.3	423	5	ABB90874 Herbicida
17	767.5	32.2	423	3	AAAG28472 Arabidops
18	767.5	32.2	423	3	AAAG25412 Arabidops
19	767.5	32.2	423	8	ADT55973 Plant pol
20	767.5	32.2	438	3	AAAG28471 Arabidops
21	767.5	32.2	438	3	AAAG25411 Arabidops
22	766.5	32.1	423	3	AAAG27394 Arabidops
23	766.5	32.1	438	3	AAAG27393 Arabidops
24	766	32.1	434	8	ADT59706 Plant pol

25	725.5	30.4	358	7	ABM86264 Rice abio
26	705	29.6	434	8	ADX93643 Plant ful
27	705	29.6	515	8	ADX76485 Plant ful
28	691.5	29.0	385	3	AAAG25413 Arabidops
29	691.5	29.0	385	3	AAAG28473 Arabidops
30	690.5	29.0	385	3	AAAG27395 Arabidops
31	686.5	28.8	447	3	AAAG22257 Arabidops
32	686.5	28.8	447	3	AAAG45635 Arabidops
33	686.5	28.8	447	5	ABM91949 Arabidops
34	686.5	28.8	447	5	AAU12004 Arabidops
35	686.5	28.8	529	3	AAAG45634 Arabidops
36	686.5	28.8	529	3	AAAG22256 Arabidops
37	684	28.7	448	3	AAV97307 Senescenc
38	670	28.1	515	5	ABB90883 Herbicida
39	659	27.6	472	8	ADX78298 Plant ful
40	641.5	26.9	412	3	AAAG22258 Arabidops
41	641.5	26.9	412	3	AAAG45636 Arabidops
42	616	25.8	355	5	ABM91958 Arabidops
43	610.5	25.6	397	8	ADY08595 Plant ful
44	606.5	25.4	529	5	ABM91187 Herbicida
45	580.5	24.3	195	3	AAV97303 Senescenc

## ALIGNMENTS

RESULT 1	
ID	AAV97298 standard; protein; 447 AA.
AC	AAV97298;
XX	
DT	03-JAN-2001 (first entry)
XX	
DE	Senescence-induced lipase.
XX	
KW	Senescence-induced lipase; senescence; lipase; antisense; regulation; modulation; resistance; stress; crop protection; ethylene.
XX	
OS	Dianthus caryophyllus.
XX	
PN	MO200049164-A1.
PD	
XX	24-AUG-2000.
XX	
PP	14-FEB-2000; 2000MO-US003494.
XX	
PR	16-FEB-1999; 99US-00250280.
XX	
PA	(SENE-) SENESCO INC.
XX	
FI	Thompson JE, Wang T, Hudak K, Hong Y,
XX	
DR	WPI; 2000-549277/50.
DR	N-PSDB; AAAS3880.
XX	
PT	DNA encoding carnation senescence-induced lipase, useful for regulating the expression of senescence in plants to delay its onset and improve plant resistance to environmental stress, thus extending shelf-life or growth period.
XX	
PS	Claim 5; Page 71-72; 89pp; English.
XX	
CC	Insertion of the senescence-induced lipase coding sequence in an antisense direction in a plant genome can be used to regulate the expression of senescence in those plants. Alteration of expression of the senescence-induced lipase gene in plants results in delayed onset of senescence and improved resistance to environmental stress, thus extending the plant shelf-life and/or growth period. The genetically altered plant is useful for producing a new variety or line of plants where the alteration is stably transmitted from generation to generation. This method of regulation is advantageous over prior senescence modulating technologies since prior methods were only applicable to a

limited range of plants, e.g. to plants that are ethylene-sensitive. The antisense regulation method is applicable to all types of plants, regardless of ethylene sensitivity

Sequence 447 AA;

Query Match 100.0%; Score 2385; DB 3; Length 447;  
Best Local Similarity 100.0%; Pred. No. 3,9e-234;  
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAAEAPLGLSKPGPTPELLGSNAAGLNPDLNDELRELLRCGDFCQVYDTDFINDON 60
DB 1 MAAEAPLGLSKPGPTPELLGSNAAGLNPDLNDELRELLRCGDFCQVYDTDFINDON 60
QY 61 SSYCGSSRYGKADLLHKTAFPGADRFVVAIYATAKVSVEAFLLKSRREKMDRESN 120
DB 61 SSYCGSSRYGKADLLHKTAFPGADRFVVAIYATAKVSVEAFLLKSRREKMDRESN 120
QY 121 WIGYVVVSNDETSKVAAGREYVYVWRGTCRDYEWVDVGAQLESAPLRTQOTTHVEKV 180
DB 121 WIGYVVVSNDETSKVAAGREYVYVWRGTCRDYEWVDVGAQLESAPLRTQOTTHVEKV 180
QY 181 ENEBKSIHKSQWYDCFNINILGSASKDKGSGDDDDDDPKVMQGMWTIYTSDDPKSPF 240
DB 181 ENEBKSIHKSQWYDCFNINILGSASKDKGSGDDDDDDPKVMQGMWTIYTSDDPKSPF 240
QY 241 TKLSARFQLOTKLQKMTKRYDETLSTFAGHSIGATLSVSAFDIENLTTEIPVTAIV 300
DB 241 TKLSARFQLOTKLQKMTKRYDETLSTFAGHSIGATLSVSAFDIENLTTEIPVTAIV 300
QY 301 FGCPKVGKKRQQLFDSYPNINLVHVRNVIDLPLYPVKLMGYVNIIGIEIDSRKSTFL 360
DB 301 FGCPKVGKKRQQLFDSYPNINLVHVRNVIDLPLYPVKLMGYVNIIGIEIDSRKSTFL 360
QY 361 KDSKNPDMHNLQAILHVVSGMHGKGFVKVNRKSVLVNKSDFLKEBCLVPAMWV 420
DB 361 KDSKNPDMHNLQAILHVVSGMHGKGFVKVNRKSVLVNKSDFLKEBCLVPAMWV 420
QY 421 QNKGWVLNKGEWVLAPPEEDPTPEFD 447
DB 421 QNKGWVLNKGEWVLAPPEEDPTPEFD 447
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#### RESULT 2

AA97304 ID AA97304 standard; protein; 447 AA.

AA97304; AC

DT 03-JAN-2001 (first entry)

DB Senescence-induced lipase (Car1ip).

KW Senescence-induced lipase; senescence; lipase; antisense; regulation; modulation; resistance; stress; crop protection; ethylene.

OS Dianthus caryophyllus.

XX WO20049164-A1.

XX 24-AUG-2000.

XX 14-FEB-2000; 2000WO-US003494.

XX 16-FEB-1999; 99US-00250280.

XX (SENE-) SENESCO INC.

XX Thompson JB, Wang T, Hudak K, Hong Y;

XX WPI; 2000-549277/50.

XX DNA encoding carnation senescence-induced lipase, useful for regulating

PT the expression of senescence in plants to delay its onset and improve  
PT plant resistance to environmental stress, thus extending shelf-life or  
PT growth period.

PS Disclosure; Page 75-76; 89pp; English.

XX insertion of the senescence-induced lipase coding sequence in an  
CC antisense direction in a plant genome can be used to regulate the  
CC expression of senescence in those plants. Alteration of expression of the  
CC senescence-induced lipase gene in plants results in delayed onset of  
CC senescence and improved resistance to environmental stress, thus  
CC extending the plant shelf-life and/or growth period. The genetically  
CC altered plant is useful for producing a new variety or line of plants  
CC where the alteration is stably transmitted from generation to generation.  
CC This method of regulation is advantageous over prior senescence  
CC modulating technologies since prior methods were only applicable to a  
CC limited range of plants, e.g. to plants that are ethylene-sensitive. The  
CC antisense regulation method is applicable to all types of plants,  
CC regardless of ethylene sensitivity

XX Sequence 447 AA;

Query Match 99.7%; Score 2377; DB 3; Length 447;  
Best Local Similarity 99.8%; Pred. No. 2,6e-233;  
Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAAEAPLGLSKPGPTPELLGSNAAGLNPDLNDELRELLRCGDFCQVYDTDFINDON 60
DB 1 MAAEAPLGLSKPGPTPELLGSNAAGLNPDLNDELRELLRCGDFCQVYDTDFINDON 60
QY 61 SSYCGSSRYGKADLLHKTAFPGADRFVVAIYATAKVSVEAFLLKSRREKMDRESN 120
DB 61 SSYCGSSRYGKADLLHKTAFPGADRFVVAIYATAKVSVEAFLLKSRREKMDRESN 120
QY 121 WIGYVVVSNDETSKVAAGREYVYVWRGTCRDYEWVDVGAQLESAPLRTQOTTHVEKV 180
DB 121 WIGYVVVSNDETSKVAAGREYVYVWRGTCRDYEWVDVGAQLESAPLRTQOTTHVEKV 180
QY 181 ENEBKSIHKSQWYDCFNINILGSASKDKGSGDDDDDDPKVMQGMWTIYTSDDPKSPF 240
DB 181 ENEBKSIHKSQWYDCFNINILGSASKDKGSGDDDDDDPKVMQGMWTIYTSDDPKSPF 240
QY 241 TKLSARFQLOTKLQKMTKRYDETLSTFAGHSIGATLSVSAFDIENLTTEIPVTAIV 300
DB 241 TKLSARFQLOTKLQKMTKRYDETLSTFAGHSIGATLSVSAFDIENLTTEIPVTAIV 300
QY 301 FGCPKVGKKRQQLFDSYPNINLVHVRNVIDLPLYPVKLMGYVNIIGIEIDSRKSTFL 360
DB 301 FGCPKVGKKRQQLFDSYPNINLVHVRNVIDLPLYPVKLMGYVNIIGIEIDSRKSTFL 360
QY 361 KDSKNPDMHNLQAILHVVSGMHGKGFVKVNRKSVLVNKSDFLKEBCLVPAMWV 420
DB 361 KDSKNPDMHNLQAILHVVSGMHGKGFVKVNRKSVLVNKSDFLKEBCLVPAMWV 420
QY 421 QNKGWVLNKGEWVLAPPEEDPTPEFD 447
DB 421 QNKGWVLNKGEWVLAPPEEDPTPEFD 447
```

#### RESULT 3

AAU11997 ID AAU11997 standard; protein; 447 AA.

AAU11997; AC

DT 09-APR-2002 (first entry)

DE Carnation senescence-induced lipase.

XX Plant; senescence-induced lipase; regulation of senescence;

XX environmental stress; carnation; enzyme.

XX Dianthus caryophyllus.



PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 23-JUN-1999; 99US-0140695P.  
PR 24-JUN-1999; 99US-0140823P.  
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Best Local Similarity 56.0%; Pred. No. 1.7e-124; DB 3; Length 412;  
Matches 242; Conservative 72; Mismatches 91; Indels 27; Gaps 4;

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DB 7 SMEELISGKMWDTLPLDGLSRLRLRCGDFCQATYDAFVNDGNSKYCGASRYGKSSFF 66  
QY 76 HKTAPPGGADRFDDVAYIYATKYSVBPAPFLKRSRKREKMDRESNWIGYVVVSNDETSRV 135  
DB 67 DKVMELENSD-YEVVNFYIATARVSLPEGLLOSQSRBDSMDRESNWFGYIAVTSDESKA 125



**SQ** Sequence 412 AA;

Matches 242; Conservative 72; Mismatches 91; Indels 27; Gaps 4;

[illegible]

Db 281 VMSHKRLKLTHTNTIDLLTRYPGGLLEYVDIGINPVIDTKKSPFLSDSRNPGDMHNLQA 340

Qy 375 ILHVSGMHGVKGEKRVNKRVSVALVNSCDPLKEBCLVPPAMVNVONKGMTLNKDEMY 434

Db 341 MLHVVGNNKNGKGEFELTKMRISALVNSCEFLAECIVPGSMWVERNKGILKNDEMY 400

Qy 435 LAPPEEDPTPEF 446

Db 401 LAPVEEPVPEF 412

PT stress.

CC This invention describes a method resulting in a novel transformed plant

CC isoleucine, iso-maltose, isopentenyl pyrophosphate, leucine, lignoceric



DE ALABAMA PROCES IN NO: 55750.

PR 21-JUN-1999; 99US-0139817P

XX DE Aprobado

DE Arabidopsis thaliana protein fragment SEQ ID NO: 35450

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PR 01-JUL-1999; 99US-0141842P.  
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DB 13 SWEELIGSKMWDITLIDPDQSLRELILKCGDFCOATYAFVNDQSKYCGASRYKSSRF 72  
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QY 196 CPNINLGSASKDKGSGDDDDDDPKYMOGMMTLYTSEDPKSPRTKLSARTOLCTKXO 255  
DB 184 -----SDSDEBEGCYMLGLWLTLYTISNHPESKFTKLSLNSQLAKIKX 226  
QY 256 LMTKYKDETLSTTFAGHSIGATLSVSAFDIVEN-LTTEIPYTAVFSGCPKVGKKFPOL 314  
DB 227 LILKTKDKKPSIVLTGHSIGTEAVLAIYDIAENSSSDVVTALVFCCPGVGNKEFFDE 286  
QY 315 FDSYFNILNVLHVRNVIDILPYPVKLMGYNIGIELISDRKSTFLKDSKNPSDWHNLQA 374

Db 287 VMSHKNLKIHLVNRITDILTRYPGCLGYVDIGINFVDTKSPFLSPSRPGDMHNLQA 346  
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PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 14-OCT-1999; 99US-0159584P.
PR 18-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

```

Query Match 45.4%; Score 1082; DB 3; Length 343;  
 Best Local Similarity 55.5%; Pred. No. 3.6e-101;  
 Matches 202; Conservative 63; Mismatches 73; Indels 26; Gaps 3;

```

QY 84 ADRFDVAVLYATPAKVSPEAFILKSRREKMDRESNWTGVVVSNDPESRVAGREVVY 143
Db 5 ASDYEYVNFLYATPAKVSPEAFILKSRREKMDRESNWTGVVVSNDPESRVAGREVVY 64
QY 144 VMRGTCDEYEMVDYLGQLESAPHLRTQOTTHVEKENEKKS IHKSSWDCENILG 203
Db 65 ALRGTSNRYEMVNLGAPTSADPLHGP-----EQSGGVEGTFD----- 108
QY 204 SASKDKGSGDDDDDDPKYMGWMTIYTSDEPKSPPTKLSARTOLQTKOLMTKYXDE 263
Db 109 -----SDSEBECCKMGLITITSNHPESKTKLSLSQILAKIKELLKYXDE 159
QY 264 TLTSTFAGSLGATLSVASAPDIYEN-LTTEIPTAVPFCGPKGKNGKFOOLPSTYNLN 322
Db 160 KPSIVLTGSLGATEAVLAAYIAENSGSDVPVTAIVFCPOVGNEFRDEVSHKULK 219
QY 323 VLVHVNITDILPLYVPLMGVNVNIGIELEIDRSSTFKOSKNSPDHNIQALIHVSGW 382
Db 220 ILHVRNTIDILTRYPGGLGVVDGINFVIDTKSPFLSDSRNGDMHNLQAMLVVAGW 279
QY 383 HGVGGEFVVKRSVALVNSCDFLKEECVPPAMVYVQNKGVNLKGEWVLAPEEDP 442
Db 280 NGKKGFERKLVKRSIALVNSCEFLKAECLVPGSWVWEKOKGLIKNEDGEVLAPEEPP 339
QY 443 TPEF 446
Db 340 VPEF 343

```

RESULT 10  
 ID AAY97308 standard; protein, 348 AA.  
 AC AAY97308;  
 DT 03-JAN-2001 (first entry)  
 DE Arabidopsis EST showing 55/5% homology with senescence induced.  
 XX Senescence-induced lipase; senescence; lipase; antisense; regulation;  
 KW modulation; resistance; stress; crop protection; ethylene.  
 OS Arabidopsis thaliana.  
 PN W0200049164-A1.  
 PD 24-AUG-2000.  
 PF 14-FEB-2000; 2000WO-US003494.  
 PR 16-FEB-1999; 99US-00250280.  
 PA (SENE-) SENESCO INC.  
 PI Thompson JE, Wang T, Hudak K, Hong Y;  
 DR WPI; 2000-549277/50.  
 DR N-PSDB; AAA53885.  
 XX DNA encoding carnation senescence-induced lipase, useful for regulating  
 PT the expression of senescence in plants to delay its onset and improve  
 PT plant resistance to environmental stress, thus extending shelf-life or  
 PT growth period.  
 PS Disclosure; Fig 13; 89pp; English.  
 XX Insertion of the senescence-induced lipase coding sequence in an  
 CC antisense direction in a plant genome can be used to regulate the  
 CC expression of senescence in those plants. Alteration of expression of the  
 CC senescence-induced lipase gene in plants results in delayed onset of  
 CC senescence and improved resistance to environmental stress, thus  
 CC extending the plant shelf-life and/or growth period. The genetically  
 CC altered plant is useful for producing a new variety or line of plants

CC where the alteration is stably transmitted from generation to generation.  
 CC This method of regulation is advantageous over prior senescence  
 CC modulating technologies since prior methods were only applicable to a  
 CC limited range of plants, e.g. to plants that are ethylene-sensitive. The  
 CC antisense regulation method is applicable to all types of plants,  
 CC regardless of ethylene sensitivity

XX Sequence 348 AA;

Query Match 45.2%; Score 1077; DB 3; Length 348;  
 Best Local Similarity 55.2%; Pred. No. 1.2e-100;  
 Matches 201; Conservative 63; Mismatches 74; Indels 26; Gaps 3;

84 ADPRDVAVLYATKAVSVPKAFILKSRREKMDRESNMWIGVVVSNDETSRVARRREYV 143  
 10 ASDVEVNFYATKRVSLPBGILLQOSRDMDESNMFGIATVSDERSKALGRREIYI 69  
 144 VWRGTCRDYEMVDVLAQLESAPHLRTQOTTHVEKVENEKSIHKSWMYDCFNINLIG 203  
 70 ALKGTSHNYEMVNLGARPTSDPLHGP-----EQDGGGVVGTTFD----- 113  
 204 SASDKDKGSDDDDDPKVMQGMITYTSEDPKSPPTKLSARTOLOTKLKQMTKTKDE 263  
 114 -----SDSEDEBCKMVLGWLITTYTSNHPEKFTKLSLSQLAKIKELLLKTKYDE 164  
 264 TLTSTFAGHSIGATLSVSAFDIVEN-LTTEIPTAVVFCGCPKVGKFKQQLPFSYNLN 322  
 165 KPSTVLTGHSIGPTEAVLAADIAENSSDDVPVTAIVFGCPQVGNKEFDEVNSHKLK 224  
 323 VLHVRNVIDLIPYPVKLMGVNIGIELIDSRKSTFLKDSKNPSDMHNLQAILHVVSGW 382  
 225 ILHVRNTIDLTTRPGSLGVVDIGINPVIDTKSPFLSDSRNPGDHNILQAMLVVAGW 284  
 383 HGKGEFKNVKNKSVALVNSCDFLKEECVLPAMVNVQNKGMVLNKGEMVLAPPEEDP 442  
 285 NGKKGEFKLMVKRSIALVNSCEFLKAECLVPGSMWVEKNKGLIKNEDGEVTLAPVEEP 344  
 443 TPEF 446  
 345 VPEF 348

RESULT 11

ID AAU12003 standard; protein; 348 AA.

XX AAU12003;

DT 09-APR-2002 (first entry)

DE Carnation senescence-induced lipase-like protein from Arabidopsis.  
 XX Plant; senescence-induced lipase; regulation of senescence;  
 KM environmental stress; carnation; enzyme.  
 XX

OS Arabidopsis sp.

PN WO200198510-A2.

PD 27-DEC-2001.

PF 19-JUN-2001; 2001WO-US019385.

XX 19-JUN-2000; 2000US-00597774.

PR 05-JUL-2000; 2000US-00610104.

XX (SENESC-) SENESCO TECHNOLOGIES INC.

PI Thompson JE, Wang T, Hudak K, Hong Y;

DR WPI; 2002-130793/17.

XX N-PSDB; AAS20756.

PT New carnation and Arabidopsis genes encoding a senescence-induced lipase,  
 PT useful for controlling (onset of) senescence in plants, regulating  
 PT expression of senescence in plants, or modifying senescence in transgenic  
 PT plants.

XX Disclosure; Fig 13; 106pp; English.

CC The present invention relates to the isolation of polynucleotide  
 CC sequences encoding plant (carnation and Arabidopsis) senescence-induced  
 CC lipases. Regulation of expression of senescence in plants is obtained by  
 CC integration of a gene or gene fragment encoding senescence-induced lipase  
 CC into the plant genome. The isolated polynucleotide sequences are useful  
 CC for controlling senescence or the onset of senescence in plants caused by  
 CC either internal or external factors (e.g. environmental stress), or  
 CC regulating expression of senescence in plants. The DNAs are also useful  
 CC for modifying senescence in transgenic plants. The present sequence  
 CC represents a partial Arabidopsis protein which shares 55.5% homology with  
 CC the carnation senescence-induced lipase

XX Sequence 348 AA;

Query Match 45.2%; Score 1077; DB 5; Length 348;  
 Best Local Similarity 55.2%; Pred. No. 1.2e-100;  
 Matches 201; Conservative 63; Mismatches 74; Indels 26; Gaps 3;

84 ADPRDVAVLYATKAVSVPKAFILKSRREKMDRESNMWIGVVVSNDETSRVARRREYV 143  
 10 ASDVEVNFYATKRVSLPBGILLQOSRDMDESNMFGIATVSDERSKALGRREIYI 69  
 144 VWRGTCRDYEMVDVLAQLESAPHLRTQOTTHVEKVENEKSIHKSWMYDCFNINLIG 203  
 70 ALKGTSHNYEMVNLGARPTSDPLHGP-----EQDGGGVVGTTFD----- 113  
 204 SASDKDKGSDDDDDPKVMQGMITYTSEDPKSPPTKLSARTOLOTKLKQMTKTKDE 263  
 114 -----SDSEDEBCKMVLGWLITTYTSNHPEKFTKLSLSQLAKIKELLLKTKYDE 164  
 264 TLTSTFAGHSIGATLSVSAFDIVEN-LTTEIPTAVVFCGCPKVGKFKQQLPFSYNLN 322  
 165 KPSTVLTGHSIGPTEAVLAADIAENSSDDVPVTAIVFGCPQVGNKEFDEVNSHKLK 224  
 323 VLHVRNVIDLIPYPVKLMGVNIGIELIDSRKSTFLKDSKNPSDMHNLQAILHVVSGW 382  
 225 ILHVRNTIDLTTRPGSLGVVDIGINPVIDTKSPFLSDSRNPGDHNILQAMLVVAGW 284  
 383 HGKGEFKNVKNKSVALVNSCDFLKEECVLPAMVNVQNKGMVLNKGEMVLAPPEEDP 442  
 285 NGKKGEFKLMVKRSIALVNSCEFLKAECLVPGSMWVEKNKGLIKNEDGEVTLAPVEEP 344  
 443 TPEF 446  
 345 VPEF 348

RESULT 12

ID ABW86048 standard; protein; 510 AA.

XX ABW86048;

DT 02-JUN-2005 (first entry)

DE Rice abiotic stress responsive polypeptide SEQ ID NO:4294.

XX abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.

OS Oryza sativa.

PN WO2003008540-A2.

XX 30-JAN-2003.

XX 21-JUN-2002; 2002WO-US019668.

XX 22-JUN-2001; 2001US-0300112P.  
 PR 24-AUG-2001; 2001US-0314662P.  
 PR 26-SEP-2001; 2001US-0325277P.  
 PR 21-NOV-2001; 2001US-0332132P.

XX (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX Kreppe J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,  
 PI Moughamer T, Provart N, Ricke D, Zhu T;  
 XX WPI; 2003-248011/24.

XX New stress-responsive nucleic acid, useful for altering the  
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold  
 PT stress, salt stress or osmotic stress.

XX Claim 1; SEQ ID NO 4294; 89pp; English.

XX The invention relates to novel abiotic stress responsive polynucleotides  
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host  
 CC cells, and plants containing such polynucleotides. Also disclosed are  
 CC methods for using the polynucleotides and polypeptides to alter the  
 CC responsiveness of a plant to abiotic stress. The invention is useful in  
 CC agriculture. The nucleic acid is useful for determining whether a test  
 CC plant has been exposed to an abiotic stress condition. It is also useful  
 CC for selecting an agent that alters abiotic stress regulated  
 CC polynucleotide expression in a plant cell, and to identify a homolog or  
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid  
 CC molecule and the polypeptide encoded by it are useful in altering the  
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt  
 CC stress, osmotic stress or any of their combinations. The present sequence  
 CC is used in the exemplification of the invention

XX Sequence 510 AA;

Query Match 44.2%; Score 1054; DB 7; Length 510;  
 Best Local Similarity 46.8%; Pred. No. 4.9e-98;  
 Matches 206; Conservative 72; Mismatches 110; Indels 52; Gaps 6;

QY 11 SKPGTWELLIGSNAGLPLNDELRLRCDFQVYTYDTINDQNSYCGSSXYG 70

DB 71 SRP---WPELLIGSAMHMDLPLDLTLRLRLILCGDLQVYDYSFNSHSHRYCOTCFPS 127

QY 71 KADLIHKAFPGAGRPDVAVYLVATKAVSPEARFLKRSREKKDRSNNMGYVVSND 130

DB 128 RSTLDRQFPAGD-LSVAALVATSDATAPFGSMVYSMSKSNMIGYAVASND 186

QY 131 ETSRVAGREVVVWRGTCRDYEWVVLGAQLESAPLRLTQOTTHVEKVENEEKSIHK 190

DB 187 AAAAASGGRVIVYVAMRGTRISLEWVDVLPD-----VHDH----- 223

QY 191 SSWYDFCNINILGASAKDKGSDDDDDPKVWOGMTIYSEDPKSPFTYKLSARTOLQ 250

DB 224 -----LLEPGHPGFRS-----RVMGMWLIYSSTDERSPFSKYSRARDML 264

QY 251 TKLQKMTKYDETSTIFAGHSIGATISVSAPIVENLUTR-----IPTAVVFGCP 304

DB 265 AAVRELVARYNRESIGVCTGHSIGASLATTLCAPDIVVNGSVKVDGAHPTAVVFGSP 324

QY 305 KVNKKFPQOLFDSYNNLVAVLRNVYIDLPLTPYVKLMGVNIGIELEIDRSKSTFLKDSK 364

DB 325 QIGNEFFKKQPEQGNLRALHVRNMPDLPLTPYPSGLIGAVNGKTLQVDSKSPYVKGDT 384

QY 365 NPSDMHNLQAILHAVVSGMHVGGEFRVNVKRSVALVNNKSCDFLKEECVLPAMVYVONGK 424

DB 385 SPGDYHNLQGIILHTVAGMNGKGEFKLQVRSVALVNNKSGFLKDSNLVPSMWYERNKG 444

QY 425 MYLNDGEMVLAPPEDDPTP 444

DB 445 MYLGNGEMQLEGPAAENLP 464

RESULT 13

ID ADV24723 standard; protein; 410 AA.

XX ADV24723;

DT 21-APR-2005 (first entry)

DE Plant full length insert polypeptide seqid 72507.

KM plant protectant; plant growth regulator; gene therapy; plant;  
 KM recombinant DNA construct; physical array; plant breeding marker;  
 KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KM growth rate; cell cycle pathway; disease resistance;  
 KM galactomannan production; lignin production; plant growth regulator;  
 KM yield; plant growth; plant development; seed oil; protein yield;  
 KM protein content.

XX Unidentified.

OS US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

PR 06-MAY-1999; 99US-00304517.

PR 05-NOV-2001; 2001US-00985678.

XX (LIU/J.) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D K.

XX (SCRE/) SCREEN S E.

XX (TABAS/) TABASKA J E.

XX (CAO/) CAO Y.

PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

PT New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.

XX Claim 1; SEQ ID NO 72507; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a  
 XX polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.secdat.uspco.gov/sequence.html?docid:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This is the amino acid sequence of a plant full length insert  
 CC polypeptide that can be used in the recombinant DNA construct of the  
 CC invention.

XX Sequence 410 AA;

Query Match 34.6%; Score 824.5; DB 8; Length 410;

Best Local Similarity 39.5%; Pred. No. 9.9e-75;

Matches 172; Conservative 70; Mismatches 144; Indels 49; Gaps 5;

QY 9 GLSKPPTWELLGSSNAGLPLNDELRELLRCGDFCCQVYDTPTINDQSSYCGSSR 68  
 Db 21 GNGVAVARWKEKLNGLNWKGLVDPDLDRNIIINGBELSGATYTGILNRRSRVYASSCL 80  
 QY 69 YGRADLLHKTAFPGGADRFVAVLYATAKVSVEPAFLKSRSEKMDRESNMIGYVVVS 128  
 Db 81 FNRDFLSRVVV-SNPMLYEITKEIYAMCTVSLPDGFMVXSLSKAAMSROSNMGMFYAVA 139  
 QY 129 NDESRVAGREVVVVRGTCRDYEMVDVGAOLESAHPLLRTOQTHVEKVENBEKSSI 188  
 Db 140 TDEKELGRDVAANRGITIRVEMVDDDISLVASEIV----- 180  
 QY 189 HKSSWYDFCNINILGSASDKGKSGDDDDDPKVMOGMMTIYTSBPKSPFTLSARTQ 248  
 Db 181 -----LPGSA-----NPCVHGMLSVTSADPGSGYNESARHQ 215  
 QY 249 LQTKLQMLTKYKDETLSTFAGSLGATLSVSAFDIVENLTTE--IPYAVVFGCPKV 306  
 Db 216 VLNEVKRIODLYKKEETSIITGHSLGALATINATIVSNGVNRSCCPVSAFVGSFPRV 275  
 QY 307 GNKKFOOLFDSYPRNLVNLVNRNVIDLPIYPVKLMGYVNIIGLEIDSRKSTFLKDSKP 366  
 Db 276 GNLDFOAFDSADRLRLRVNSPDVVPKMP--KLGYSDVGTETLMDTGESPYLKAPGNP 333  
 QY 367 SDMNLQAILHVVSGMHGVKGEFFKVNRKSVAVLNKSCDFLKEECLVPPAMVYQNKGMV 426  
 Db 334 LTHWDMCYHGVAGAGSGSGFELVDRVALVNXKIEDALRNFAVPPSMVYQNKGMV 393  
 QY 427 LNKDEWVTLAPPEED 441  
 Db 394 KGKXGRWHLADHEED 408

## RESULT 14

ABB92980  
 ID ABB92980 standard; protein; 419 AA.  
 AC ABB92980;  
 XX  
 DT 31-MAY-2002 (first entry)  
 DE Herbicidally active polypeptide SEQ ID NO 2191.  
 KM Herbicidal; plant; agriculture; herbicide.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN MO200210210-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 28-AUG-2001; 2001MO-EP009892.  
 XX  
 PR 28-AUG-2001; 2001MO-EP009892.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 PI Tietjen K, Weidler M;  
 XX  
 DR WPI; 2002-269010/31.  
 XX  
 PT Identifying plant target proteins for herbicidally active compounds,  
 PT comprising aligning and comparing nucleic acid or amino acid sequences  
 PT from plant with nucleic acid or amino acid sequences from non-plant  
 PT organisms.  
 XX  
 PS Claim 5; SEQ ID NO 2191; 261pp + Sequence Listing; English.  
 XX  
 CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
 CC for herbicidally active compounds, comprising aligning and comparing  
 CC nucleic acid or amino acid sequences from plant with nucleic acid or  
 CC amino acid sequences from non-plant organisms using suitable search  
 CC parameters, where plant sequences having an E-value greater by a factor

CC of 3 than the E-value of most similar non-plant sequences are selected.  
 CC The polypeptides or nucleic acids encoding them are useful for  
 CC identifying modulators. The identified modulators are useful as  
 CC herbicides

XX Sequence 419 AA;

Query Match 33.1%; Score 789.5; DB 5; Length 419;  
 Best Local Similarity 37.8%; Pred. No. 3.8e-71;  
 Matches 168; Conservative 77; Mismatches 137; Indels 63; Gaps 8;

QY 17 WPELLGSNAGLPLNDELRELLRCGDFCCQVYDTPTINDQSSYCGSSRYKADLLH 76  
 Db 23 WRDLSGQNMHKMGMLQPDQLREYIIHYGMAQAGVDTPTNINTESQFAGASIVRKQFPA 82  
 QY 77 KT-----AFPGADRFVAVLYATAKVSVEPAFLKSRSEKMDRESNMIGYVVVSDET 132  
 Db 83 KVGLEIAPH--YTKYKTKETIYATSDIHVESFLPISREGWSKESNMGGYAVATDQG 140  
 QY 133 SRVAGREVVVVRGTCRDYEMVDVGAOLESAHPLLRTOQTHVEKVENBEKSSIHKSS 192  
 Db 141 TALGRDIIYVSMKGSVQPLEWEDFEFGLVNA----- 173  
 QY 193 WYDFCNINILGSASDKGKSGDDDDDPKVMOGMMTIYTSBPKSPFTLSARTQLTK 252  
 Db 174 -----IKIG-----BRNDQVQHGMWYSIVNSODERSPFTTNADQVIRE 215  
 QY 253 LKQMLTKYKDETLSTFAGSLGATLSVSAFDIVEN-----LTTEIPYAVVFGCP 304  
 Db 216 VGRLEEKYKDEEVSITTCGHSLGALATLSATIVANGVNRPKSRPDKSCPVAFAVFPASP 275  
 QY 305 KVNKKFOOLFDSYPRNLVNLVNRNVIDLPIYPVKLMGYVNIIGLEIDSRKSTFLKDSK 364  
 Db 276 KVGSDPRKLFSGLEDIRVRLTRLPDVIPIPP--IGISVGDDEFIDTRKSPYMKSPG 333  
 QY 365 NPSDMNLQAILHVVSGMHGV-KGE-FKVNRKSVAVLNKSCDFLKEECLVPPAMVYQNKGMV 422  
 Db 334 NLATFHLEGYLHGVAGTGTGNKADLFRLDVERAIGLVNKSVDGLKDCMCPGKMRVTKN 393  
 QY 423 KGVNLKDGWVTLAPPEEDPTPEED 447  
 Db 394 KGMAQODGSMELVDHEIDNEDLD 418

## RESULT 15

AA97305  
 ID AA97305 standard; protein; 418 AA.  
 AC AA97305;  
 XX  
 DT 03-JAN-2001 (first entry)  
 DE Senescence-induced lipase (arl1p).  
 XX  
 KM Senescence-induced lipase; senescence; lipase; antisenescence; regulation;  
 KW modulation; resistance; stress; crop protection; ethylene.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN MO200049164-A1.  
 XX  
 PD 24-AUG-2000.  
 XX  
 PF 14-FEB-2000; 2000MO-US003494.  
 XX  
 PR 16-FEB-1999; 99US-00250280.  
 XX  
 PA (SENE-) SENESCO INC.  
 XX  
 PI Thompson JE, Wang T, Hudak K, Hong Y;  
 XX  
 DR WPI; 2000-549277/50.

PT DNA encoding carnation senescence-induced lipase, useful for regulating the expression of senescence in plants to delay its onset and improve plant resistance to environmental stress, thus extending shelf-life or growth period.

PS Disclosure; Page 76-78; 89pp; English.

Insertion of the senescence-induced lipase coding sequence in an antisense direction in a plant genome can be used to regulate the expression of senescence in those plants. Alteration of expression of the senescence-induced lipase gene in plants results in delayed onset of senescence and improved resistance to environmental stress, thus extending the plant shelf-life and/or growth period. The genetically altered plant is useful for producing a new variety or line of plants where the alteration is stably transmitted from generation to generation. This method of regulation is advantageous over prior senescence modulating technologies since prior methods were only applicable to a limited range of plants, e.g. to plants that are ethylene-sensitive. The antisense regulation method is applicable to all types of plants, regardless of ethylene sensitivity.

**SD Sequence 418 AA;**

Query Match	32.5%;	Score 775;	DB 3;	Length 418;
Best Local Similarity	37.5%;	Pred. No. 1.2e-69;		
Matches 167; Conservative	76;	Mismatches 138;	Indels 64;	Gaps 9;

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Qy 17 PPELLGSNMAQLLPIPNDELRELLRCQDFCQVYTDTPINDQNSYCGSSRGXKADLLH 76
Db 23 WRDLGQNHWMKMLPDLDDLEBYIIHYGBMAQADTFENINTESQFAGASITYSRKDFEFA 82
Qy 77 KT----AEPGADRFPDVVAUYLYATAKVSPBEAFLLSRSREKMDRESNMVIGYVVSNDET 132
Db 83 KYGLEIAHP--YTKYKVTKFATASDIHVPESFLPLPISREGMKSBNMVGVAVTDQG 140
Qy 133 SRVAGREYVYVWRCICRDYEWYDVLGAQLESHPLLRTQOTTHVEKVENBKSSIHKS 192
Db 141 TALLRERDVLVWMRGSGVQPLEWEDEFEGLVNA----- 173
Qy 193 WYDFCNINILGSASKDKGSGDDDDDDDPKVMGMMTIYTSBDPKSPFTYLSARTOLQTK 252
Db 174 -----IKIFG-----ERNDQVQIHQWVSIYMSQBERSFTYTNARDQVLR 215
Qy 253 LKQMLTKYKDEFTLSTFAGHSIGATLSSVSAFDIVEN-----LTLEIPVAVVFGCP 304
Db 216 VGRLEEKYKDEEVSITICHSISGAALATQSAIDIVANGYNRPKSRPDKSPVIAFPASP 275
Qy 305 KYGNKKKFOOLFDSYPLNVLNHNVNDLPLYPVKLMGYNIGIELEIDRSKSTFLDSK 364
Db 276 RKGSDSDFRKLFGSLEDIRVLRTRNLSDVPIYPP--IGYSEVDEFDIDTRKSPYMKSPG 333
Qy 365 NPSDMHNLQAILHHVVSQMGHV--KGE-FKVVNKSVALVNKSCDFLKEBCLVPAMWVON 422
Db 334 NLATFHLCLEGYLHGVAGTOGTNKADFLRLDVERAIGLVNKSVDGLKDECMVPGKMRVLKN 393
Qy 423 KGMVNLKQSEWVLAPPEBDPTPEFD 447
Db 394 KQ-AQODDGSWELVHDIEDNEJLD 417

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